GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 11, 2002, 09:26:45 ; Search time 66.82 Seconds
(without alignments)
3769.900 Million cell updates/sec

Title: US-09-528-031-2
Perfect score: 7308
Sequence: 1 MKDIDIGKEYIIPSPGYRSV.....DSSRFYAMFAAAENKVAVKG 1437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 528882 seqs, 175299045 residues

Total number of hits satisfying chosen parameters: 528882

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7297	99.8	1437	6	US-10-162-012-38	Sequence 38, Appl
2	7293	99.8	1437	5	US-09-647-140A-4	Sequence 4, Appli
3	7293	99.8	1437	6	US-10-154-452-2	Sequence 2, Appli
4	7285	99.7	1437	7	US-60-389-987-563	Sequence 563, App
5	6674	91.3	1325	6	US-10-154-452-6	Sequence 6, Appli
6	2663.5	36.4	1382	6	US-10-087-782A-31	Sequence 31, Appl
7	2540.5	34.8	1360	6	US-10-162-012-34	Sequence 34, Appl
8	2049.5	28.0	1325	5	US-09-647-140A-2	Sequence 2, Appli
9	2034.5	27.8	1388	7	US-60-389-987-1718	Sequence 1718, Ap
10	2023.5	27.7	1510	5	US-09-935-625-26957	Sequence 26957, A
11	2023.5	27.7	1529	5	US-09-935-625-26956	Sequence 26956, A
12	2023.5	27.7	1622	5	US-09-935-625-26955	Sequence 26955, A
13	2013.5	27.6	1510	5	US-09-935-625-26574	Sequence 26574, A
14	2013.5	27.6	1529	5	US-09-935-625-26573	Sequence 26573, A
15	2013.5	27.6	1622	5	US-09-935-625-26572	Sequence 26572, A
16	1992	27.3	1499	5	US-09-935-625-3013	Sequence 3013, Ap
17	1992	27.3	1499	5	US-09-935-625-25379	Sequence 25379, A
18	1992	27.3	1530	5	US-09-935-625-3012	Sequence 3012, Ap
19	1992	27.3	1530	5	US-09-935-625-25378	Sequence 25378, A
20	1992	27.3	1623	5	US-09-935-625-3011	Sequence 3011, Ap
21	1992	27.3	1623	5	US-09-935-625-25377	Sequence 25377, A
22	1988	27.2	1507	5	US-09-935-625-3328	Sequence 3328, Ap
23	1988	27.2	1507	5	US-09-935-625-26043	Sequence 26043, A
24	1988	27.2	1538	5	US-09-935-625-3327	Sequence 3327, Ap
25	1988	27.2	1538	5	US-09-935-625-26042	Sequence 26042, A
26	1988	27.2	1631	5	US-09-935-625-3326	Sequence 3326, Ap
27	1988	27.2	1631	5	US-09-935-625-26041	Sequence 26041, A
28	1984.5	27.2	1494	7	US-60-360-039-6697	Sequence 6697, Ap
29	1983.5	27.1	1515	7	US-60-360-039-1637	Sequence 1637, Ap
30	1941	26.6	1527	5	US-09-647-140A-6	Sequence 6, Appli
31	1923	26.3	1581	6	US-10-179-131-6804	Sequence 6804, Ap
32	1897	26.0	1573	7	US-60-360-039-6867	Sequence 6867, Ap
33	1897	26.0	1573	7	US-60-360-039-6868	Sequence 6868, Ap
34	1896.5	26.0	1508	7	US-60-360-039-4104	Sequence 4104, Ap
35	1874.5	25.6	1444	7	US-60-360-039-2241	Sequence 2241, Ap
36	1828	25.0	1355	5	US-09-935-625-7277	Sequence 7277, Ap
37	1828	25.0	1355	5	US-09-935-625-16233	Sequence 16233, A
38	1819.5	24.9	1516	5	US-09-935-625-5376	Sequence 5376, Ap
39	1819.5	24.9	1516	5	US-09-935-625-8196	Sequence 8196, Ap
40	1819.5	24.9	1516	5	US-09-935-625-20409	Sequence 20409, A
41	1819.5	24.9	1516	5	US-09-935-625-25430	Sequence 25430, A
42	1806	24.7	1251	5	US-09-935-625-5377	Sequence 5377, Ap
43	1806	24.7	1251	5	US-09-935-625-8197	Sequence 8197, Ap
44	1806	24.7	1251	5	US-09-935-625-20410	Sequence 20410, A
45	1806	24.7	1251	5	US-09-935-625-25431	Sequence 25431, A

ALIGNMENTS

RESULT 1
US-10-162-012-38
; Sequence 38, Application US/10162012
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11

```
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 1437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-012-38


  Query Match           99.8%;  Score 7297;  DB 6;  Length 1437;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1435;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
          ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840

Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437


RESULT   2
US-09-647-140A-4
; Sequence 4, Application US/09647140A
; GENERAL INFORMATION:
;  APPLICANT: Fox Chase Cancer Center
;  APPLICANT:  Kruh, Gary D.
;  APPLICANT:  Lee, Kun
;  APPLICANT:  Belinsky, Martin G.
;  APPLICANT:  Bain, Lisa J.
;  TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
;  TITLE OF INVENTION:  Nucleic Acids and Methods of Use Thereof
;  FILE REFERENCE: FCCC 98-02
;  CURRENT APPLICATION NUMBER: US/09/647,140A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: PCT/US99/06644
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,759
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/095,153
;  PRIOR FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 1437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-647-140A-4


  Query Match           99.8%;  Score 7293;  DB 5;  Length 1437;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1434;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
```

```
Db       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
Db      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120
Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Db     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Db     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Qy     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Qy     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Qy     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
Db     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQGITVGVAPIVVVIASVVTFSV 420
Qy     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Db     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Qy     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Db     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Qy     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
Db     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
Qy     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Db     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Qy     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Db     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Qy     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Db     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Qy     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
Db     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840
Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
Db     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
Db     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
Db     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
Qy    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
Db    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
Qy    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
Db    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
Qy    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
Db    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
Qy    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
Db    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
Qy    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
Db    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
Qy    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
Db    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
Qy    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
Db    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
```

RESULT 3
US-10-154-452-2
; Sequence 2, Application US/10154452
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Roy, Josee
; APPLICANT: Connop, Bruce P.
; TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
; TITLE OF INVENTION: EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
; TITLE OF INVENTION: DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
; FILE REFERENCE: 100103.420
; CURRENT APPLICATION NUMBER: US/10/154,452
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-452-2

Query Match 99.8%; Score 7293; DB 6; Length 1437;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1434; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Db       1 MEDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
Db      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120
Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Db     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Db     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Qy     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Qy     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
```

```
Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
          ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840

Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
```

```
RESULT   4
US-60-389-987-563
; Sequence 563, Application US/60389987
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465P2
;  CURRENT APPLICATION NUMBER: US/60/389,987
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 3025
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
;   LENGTH: 1437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-389-987-563
```

Query Match 99.7%; Score 7285; DB 7; Length 1437;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1433; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCPTRLI 180

Qy    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
```

```
Qy     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
           ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840

Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 MLNIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
```

```
RESULT    5
US-10-154-452-6
; Sequence 6, Application US/10154452
; GENERAL INFORMATION:
;  APPLICANT: Reiner, Peter B.
;  APPLICANT:  Roy, Josee
;  APPLICANT:  Connop, Bruce P.
;  TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
;  TITLE OF INVENTION:  EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
;  TITLE OF INVENTION:  DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
;  FILE REFERENCE: 100103.420
;  CURRENT APPLICATION NUMBER: US/10/154,452
;  CURRENT FILING DATE:  2002-05-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1325
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-154-452-6
```

Query Match 91.3%; Score 6674; DB 6; Length 1325;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1309; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
           |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
           ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840

Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
```

```
Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECI 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECI 1312


RESULT   6
US-10-087-782A-31
; Sequence 31, Application US/10087782A
; GENERAL INFORMATION:
;  APPLICANT: AVENTIS PHARMA SA
;  APPLICANT:  US GOVERNMENT of the UNITED STATES
;  TITLE OF INVENTION: NUCLEIC ACID OF THE HUMAN ABCC11 GENE, VECTORS
;  TITLE OF INVENTION:  CONTAINING SUCH NUCLEIC ACID, AND USES THEREOF
;  FILE REFERENCE: ABCC11 GENE
;  CURRENT APPLICATION NUMBER: US/10/087,782A
;  CURRENT FILING DATE:  2002-07-03
;  PRIOR APPLICATION NUMBER: 60/272,757
;  PRIOR FILING DATE: 2001-03-05
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 1382
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-087-782A-31


  Query Match             36.4%;  Score 2663.5;  DB 6;  Length 1382;
  Best Local Similarity   40.8%;  Pred. No. 1.9e-189;
  Matches  556;  Conservative  258;  Mismatches  501;  Indels   49;  Gaps    8;

Qy      77 PKGKYHHGLSALKPIRTTCKH--QHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVW 134
           | |||   |  : | |   :     |:|||||| :| ||||: |  :   : |    :
Db      60 PWGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPL-MIQSLRSRLDENTIP 118

Qy     135 SLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGF 194
           || |::|| | :|| |||:||::  | : ||:  |:  | |||||   :  :   :|
Db     119 PLSVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTRLIFDALLGICFCIASV 178

Qy     195 SGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAI 254
           ||  ::  :|||::    |: : : |   | |:| |:| | : :| :| || :| | |:
Db     179 LGPILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAV 238

Qy     255 LTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVII 314
           : ||:|::: |::   : || |:  : |   :||    | |:       ::  | :  |
Db     239 SSFAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFI 298

Qy     315 LGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWV 374
           :| | |:    ::| :|  :| :|:    :      :|:|::  :|||| || |||| |
Db     299 IGYTAFIAILCYLLVFPLAVFMTRMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWE 358

Qy     375 KAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAF 434
           | |:: :: :| :||::||| |  ||:|     |:  :|: |   :| :|   |||: ||
Db     359 KPFAKIIEDLRRKERKLLEKCGLVQSLTSITLFIIPTVATAVWVLIHTSLKLKLTASMAF 418

Qy     435 TVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKN 494
```

```
Db     419 SMLASLNLLRLSVFFVPIAVKGLTNSKSAVMRFKKFFLQESPVFYVQTLQDPSKALVFEE 478

Qy     495 ATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSD 554
           |||:|  :  | |                                    |:  |: ||   :
Db     479 ATLSWQQTCPGIVNG----------------------------ALELERNGH-ASEGM 507

Qy     555 ERP----SPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILG 610
             ||     ||||           |   || |:| : :| ::|:||: ||||:||:||||
Db     508 TRPRDALGPEEEGNS--------LGPELHKINLVVSKGMMLGVCGNTGSGKSSLLSAILE 559

Qy     611 QMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAIL 670
           :| |||||: : |: ||| |||||::  :|:||| |  ||: ||  ||: | |  || :|
Db     560 EMHLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDKARYLQVLHCCSLNRDLELL 619

Qy     671 PSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRK 730
           |  |:|||||| ||||||:|||||||:|||| ||:|||||||:||||| |||    |:|
Db     620 PFGDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDPLSAVDAHVGKHIFEECIKK 679

Qy     731 HLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNLLLGETP 790
           |: |||: |||||||  | ::| :: | | | ||| |||   | || :   :    |
Db     680 TLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELMQKKGKYAQLIQKMHKEATS 739

Qy     791 PVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYI 850
           :  :: |     : :||              ||   | || | ||  :||: | ||  ||
Db     740 DMLQDTAKIAEKPKVESQALATSLEESLNGNAV--PEHQLTQEEEMEEGSLSWRVYHHYI 797

Qy     851 QAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVS-DSMKDNP 909
           ||||| :   :|    :| | | || ||||||::|||| :    | |      :: |||
Db     798 QAAGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQGSGTNSSRESNGTMADLGNIADNP 857

Qy     910 HMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTG 969
           : :|  :| |:  ::: :      :| | | :||: ||::|| :: | || |||| | |
Db     858 QLSFYQLVYGLNALLLICVGVCSSGIFTKVTRKASTALHNKLFNKVFRCPMSFFDTIPIG 917

Qy     970 RILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLH 1029
           |:|| |: |::::|  ||  :| |:   ::|   : ::: : |: |:    :::: : :
Db     918 RLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSPYILLMGAIIMVICFIYY 977

Qy    1030 IVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFF 1089
           :: :  |   |||:| ::||  ||| :|:|||::|| | | ::|: ::: | |
Db     978 MMFKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTEDFISQFKRLTDAQNNYLL 1037

Qy    1090 LFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRL 1149
           ||  : ||:|:||:::  :     | :       | ::  :|::  :||   || | |:
Db    1038 LFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMAVNIVLQLASSFQATARI 1097

Qy    1150 ASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLV 1209
           ||||:||:|||  |:|   ||| ::  :   ||| ||: |::  |:||:| | |
Db    1098 GLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGEIIFQDYHMKYRDNTPTV 1157

Qy    1210 LKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSK 1269
           |  :: ||:  | :|||||||||||||||||||||   | | |||| |  ||| |||||
Db    1158 LHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRILIDGVDICSIGLEDLRSK 1217

Qy    1270 LSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDN 1329
           ||:|||:||| |||:| |||||:::|: |||||||||  : : |:: | || ::|:||| |
Db    1218 LSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKAISKFPKKLHTDVVENGGN 1277

Qy    1330 FSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLH 1389
           |||||||||||||:||: ||:::|||||::| ||| ||| |||||  ||:| ||||:
Db    1278 FSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTIREAFQGCTVLVIAHRVT 1337

Qy    1390 TVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKV 1433
           |||  | |:|:  |:||||| | ||      | | |: | | : :
Db    1338 TVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSSL 1381


RESULT   7
US-10-162-012-34
; Sequence 34, Application US/10162012
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
```

```
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 1360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-012-34


  Query Match             34.8%;  Score 2540.5;  DB 6;  Length 1360;
  Best Local Similarity   39.4%;  Pred. No. 2.8e-180;
  Matches  542;  Conservative  251;  Mismatches  487;  Indels   97;  Gaps   11;

Qy      71 PKGKYHHGLSALKPIRTTCKH--QHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVW 134
           | |||    |  : | |    :     |:|||||| :| |||: |  :   :  |    :
Db       6 PWGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPL-MIQSLRSRLDENTIP 118

Qy     135 SLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGF 194
           || |::|| | :|| |||:||::  | : ||:  |:  | |||||  :  :   :|
Db     119 PLSVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTRLIFDALLGICFCIASV 178

Qy     195 SGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAI 254
           ||  ::  :|||::    |: : : |   | |:| |:| | : :| ':| || :| | |:
Db     179 LGPILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAV 238

Qy     255 LTMAFKKILKLKNIKEKSLGELINICSN------------DGQRMFEAAAVGSLLAGGP 301
           : ||:|::: |::   : ||  :||::             |   :||    | |:

Db     239 SSFAFEKLIQFKSVIHITSGEGGDICAHQLAVLQAISFFTGDVNYLFEGVCYGPLVLITC 298

Qy     302 VVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEV 361
              ::  | :  |:| | |:    ::| :|  :| :|:    :      :|:|::  :||
Db     299 ASLVICSISSYFIIGYTAFIAILCYLLVFPLAVFMTRMAVKAQHHTSEVSDQRIRVTSEV 358

Qy     362 LTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVH 421
           || || |||| | | |:: :: :              :|:|    |
Db     359 LTCIKLIKMYTWEKPFAKIIEGM-------------ESLTFCSKP-------------- 390

Qy     422 MTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKN 481
                     ||:::   | :  ::   | :|| |: :  || |||  || |
Db     391 -------GDGMAFSMLASLNLLRLSVFFVPIAVKGLTNSKSAVMRFKKFFLQESPVFYVQ 443

Qy     482 KPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAV 541
              |   :  : |||:|  :   | |                                |:
Db     444 TLQDPSKALVFEEATLSWQQTCPGIVNG-----------------------------AL 473

Qy     542 LAEQKGHLLLDSDERP----SPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSV 597
             |: ||   :   ||     ||||            |   || |:| : :| ::|:||:
Db     474 ELERNGH-ASEGMTRPRDALGPEEEGNS--------LGPELHKINLVVSKGMMLGVCGNT 524

Qy     598 GSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSV 657
           ||||:||:|||| :| |||||: : |: ||| |||||::  :|:||| |  ||: ||  |
Db     525 GSGKSSLLSAILEEMHLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDKARYLQV 584

Qy     658 LNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDA 717
           |: | |  || :||  |:|||||| |||||:|||||||:|||| ||:||||||:||
Db     585 LHCCSLNRDLELLPFGDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDPLSAVDA 644

Qy     718 HVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDY 777
           ||| |||   |:| |: ||: |||||||  | ::| :: | | | ||| |||   | |
Db     645 HVGKHIFEECIKKTLRGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELMQKKGKY 704

Qy     778 ATIFNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKG 837
           | :   :   |  :  :: |     : :||             ||   | || | ||
Db     705 AQLIQKMHKEATSDMLQDTAKIAEKPKVESQALATSLEESLNGNAV--PEHQLTQEEEME 762

Qy     838 QGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGN 897
           :||: | ||  |||||||  :   :|    :| |  | || |||||::|||  :   |
Db     763 EGSLSWRVYHHYIQAAGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQGSGTNSSRESN 822

Qy     898 ETSVS-DSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRIL 956
           |     :: ||| : :|  :| |:  ::: :      :| | | :||: ||::|| ::
Db     823 GTMADLGNIADNPQLSFYQLVYGLNALLLICVGVCSSGIFTKVTRKASTALHNKLFNKVF 882

Qy     957 RSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLV 1016
           | || |||| | ||:|| |: |::::|  ||  :| |:   ::|   : ::: : |: |:
Db     883 RCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSPYILL 942

Qy    1017 AVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHR 1076
              :::: : ::: :  |   |||:| ::||  ||| :|:|||::|| | | ::|: :
Db     943 MGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTEDFISQ 1002

Qy    1077 YQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYA 1136
           :: | |       ||  : ||:|:||:::  :    | :       | ::  :|::
Db    1003 FKRLTDAQNNYLLLFLSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMAVNIV 1062

Qy    1137 VQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFE 1196
           :||   || | |:  ||||:||:||||  |:|    |||  ::  :    ||| ||: |:
Db    1063 LQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGEIIFQ 1122

Qy    1197 NAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGV 1256
           :  |:||:| | ||  :: ||:  | :|||||||||||||||||||||   | | ||||
Db    1123 DYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRILIDGV 1182

Qy    1257 RISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLP 1316
           |  ||| |||||||:|||:||| |||:| |||||:::|: |||||||| : : |:: |
Db    1183 DICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKAISKFP 1242

Qy    1317 LKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAF 1376
           || ::|:||| |||||||||||||:|:: ||:::|||||::| ||| ||| ||||||
Db    1243 KKLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTIREAF 1302
```

```
Qy   1377 ADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKV 1433
Db   1303 QGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSSL 1359


RESULT   8
US-09-647-140A-2
; Sequence 2, Application US/09647140A
; GENERAL INFORMATION:
;  APPLICANT: Fox Chase Cancer Center
;  APPLICANT:  Kruh, Gary D.
;  APPLICANT:  Lee, Kun
;  APPLICANT:  Belinsky, Martin G.
;  APPLICANT:  Bain, Lisa J.
;  TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
;  TITLE OF INVENTION:  Nucleic Acids and Methods of Use Thereof
;  FILE REFERENCE: FCCC 98-02
;  CURRENT APPLICATION NUMBER: US/09/647,140A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: PCT/US99/06644
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,759
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/095,153
;  PRIOR FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1325
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-647-140A-2


  Query Match             28.0%;  Score 2049.5;  DB 5;  Length 1325;
  Best Local Similarity   35.4%;  Pred. No. 1.2e-143;
  Matches  489;  Conservative  254;  Mismatches  466;  Indels  171;  Gaps   33;

Qy      99 HPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELN 158
Db      11 NPLQDANICSRVFFWWLNPLFKIGHKR-RLEEDDMYSVLPEDRSQHLGEELQGFWDKEVL 69

Qy     159 EVGPDA---ASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPAFMVKHLLEYTQ------ 209
Db      70 RAENDAQKPSLTRAIIKCYWKSYLVLGIFTL-IEESAKVIQPIFLGK-IINYFENYDPMD 127

Qy     210 --ATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYR----TGVRLRGAILTMAFKKIL 263
Db     128 SVALNTAYAYATVLTFCTLI--------LAILHHLYFYHVQCAGMRLRVAMCHMIYRKAL 179

Qy     264 KLKNIK--EKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPTGFL 321
Db     180 RLSNMAMGKTTTGQIVNLLSNDVNKFDQVTVFLHFLWAGPLQAIAVTALLWMEIGISCLA 239

Qy     322 GSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFSQSV 381
Db     240 GMAVLIILLPLQSCFGKLFSSLRSKTATFTDARIRTMNEVITGIRIIKMYAWEKSFSNLI 299

Qy     382 QKIREEE---------RRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQ 432
Db     300 TNLRKKEISKILRSSCLRGMNLASFFSA-----SKIIV----FVTFTTYVLLGSVITASR 350

Qy     433 AFTVVTVFNSMTFALKVT---PFSVKSLSEASVAVDRFKSLFLMEEVHMIKNK--PASPH 487
Db     351 VFVAVTLYGAV--RLTVTLFFPSAIERVSEAIVSIRRIQTFLLLDEISQ-RNRQLPSDGK 407

Qy     488 IKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKG 547
Db     408 KMVHVQDFTAFWDK---------------------------------------------- 421

Qy     548 HLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISA 607


Db     422 -----ASETP------------------TLQGLSFTVRPGELLAVVGPVGAGKSSLLSA 457

Qy     608 ILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDL 667
Db     458 VLGELAPSHGLVSVHGRIAYVSQQPWVFSGTLRSNILFGKKYEKERYEKVIKACALKKDL 517

Qy     668 AILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSA 727
Db     518 QLLEDGDLTVIGDRGTPLSGGQKARVNLARAVYQDADIYLLDDPLSAVDAEVSRHLFELC 577

Qy     728 IRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNLLL- 786
Db     578 ICQILHEKITILVTHQLQYLKAASQILILKDGKMVQKGTYTEFLKSGID----FGSLLKK 633

Qy     787 ----GETPPV----EINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQL----E 834
Db     634 DNEESEQPPVPGTPTLRNRTFSESSVWSQQSSRPSL----KDGALESQDTENVPVTLSEE 689

Qy     835 EKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGST---AFSTWWLSYWI-KQGSGN 890
Db     690 NRSEGKVGFQAYKNYFRAGA---HWIVFIFLILLNTAAQVAYVLQDWWLSYWANKQSMLN 746

Qy     891 TTVT-RGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHD 949
Db     747 VTVNGGGNVTEKLD-------LNWYLGIYSGLTVATVLFGIARSLLVFYVLVNSSQTLHN 799

Qy     950 ELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAG 1009
Db     800 KMFESILKAPVLFFDRNPIGRILNRFSKDIGHLDDLLPLTFLDFIQTLLQVVGVVSVAVA 859

Qy    1010 VFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNK 1069
Db     860 VIPWIAIPLVPLGIIFIFLRRYFLETSRDVKRLESTTRSPVFSHLSSSLQGLWTIRAY-K 918

Qy    1070 GQEFLHRYQELLDDNQ----APFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIP 1125
Db     919 AEE---RCQELFDAHQDLHSEAWFLFLTTSRWFAVRLDAICAMFVIIVAFGSLILAKTLD 975

Qy    1126 PAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSP 1185
Db     976 AGQVGLALSYALTLMGMFQWCVRQSAEVENMMISVERVIEY-TDLEKEAPWEYQ-KRPPP 1033

Qy    1186 DWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVE 1245
Db     1034 AWPHEGVIIFDNVNFMYSPGGPLVLKHLTALIKSQEKVGIVGRTGAGKSSLISALFRLSE 1093

Qy    1246 LSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALER 1305
Db     1094 PEGK-IWIDKILTTEIGLHDLRKKMSIIPQEPVLFTGTMRKNLDPFKEHTDEELWNALRE 1152

Qy    1306 THMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETD 1365
Db     1153 VQLKETIEDLPGKMDTELAESGSNFSVGQRQLVCLARAILRKNQILIIDEATANVDPRTD 1212

Qy    1366 LLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db     1213 ELIQKKIREKFAHCTVLTIAHRLNTIIDSDKIMVLDSGRLKEYDEPYVLLQNKESLFYKM 1272


RESULT   9
US-60-389-987-1718
; Sequence 1718, Application US/60389987
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465P2
```

```
;  CURRENT APPLICATION NUMBER: US/60/389,987
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 3025
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1718
;   LENGTH: 1388
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-389-987-1718
```

Query Match 27.8%; Score 2034.5; DB 7; Length 1388;
Best Local Similarity 34.3%; Pred. No. 1.6e-142;
Matches 480; Conservative 259; Mismatches 471; Indels 189; Gaps 21;

```
Qy      85 LSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDV 144
           ::|||      ::  |  :|   | :|| |:: |  |   :  |   |:|||:| ::|:
Db      92 MTALK------ENPCPESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQ 144

Qy     145 NCRRLERLWQEELNEV----------GPDAA----------------------------S 166
           | : |::|  :              | |                              |
Db     145 VVPVLVKNWKKECAKTRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPS 204

Qy     167 LRRVVWIFCRTRLILSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLL 226
           | :|::       ::|     |  |  |||| ::| |:::   |:.          : |
Db     205 LFKVLYKTFGPYFLMSFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLF 263

Qy     227 LTEIVRSWSLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDG 284
           :|  :::  |   : : : :|:|:: |::   ::| | : |   ||  :||::|: | |
Db     264 VTACLQTLVLHQYFHICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDA 323

Qy     285 QRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFR 344
           ||  : |   :::   |:  || :    : |||:   | || :|  |     :  |  ::
Db     324 QRFMDLATYINMIWSAPLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQ 383

Qy     345 RKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVG 404
           : : | |:: |||:|  || :|:|||  ||   |  ||:|| ::|:|: |  ::
Db     384 VAHMKSKDNRIKLMNEILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTF 443

Qy     405 VAPIVVVIASVVTFSVHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASV 462
                : :: ||:|::|:  :  | |  ||  : :|| : | | :  : |: :|||
Db     444 TWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASV 503

Qy     463 AVDRFKSLFLMEEVH--MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMK 517
           :: | :     ||:    |: :|        | ::|||  |
Db     504 SLKRLRIFLSHEELEPDSIERRPVKDGGGTNSITVRNATFTW---------------- 545

Qy     518 KDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRT 577
                                          | |                  |
Db     546 ------------------------------------ARSDPP----------------T 552

Qy     578 LHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNA 637
           |: |   | || || : | || ||:||:||:| :|  :|| :|| |: ||| ||||| |
Db     553 LNGITFSIPEGALVAVVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQND 612

Qy     638 TLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLAR 697
           :||:|||||  : :|  | ||: :| | ||| |||| | |||||:| ||||||:||:||||
Db     613 SLRENILFGCQLEEPYYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLAR 672

Qy     698 ALYSDRSIYILDDPLSALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIF 755
           |:||:  ||: |||||:|||||| ||| : |  :  ||:|| : ||| : ||   | :|
Db     673 AVYSNADIYLFDDPLSAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIV 732

Qy     756 MKEGCITERGTHEELMNLNGDYATIF------------------------------NNL 784
           |  | |:| |:::||:  :| :|                                | :
Db     733 MSGGKISEMGSYQELLARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGM 792

Qy     785 LL----GETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
           |:    |:    :::|    ||  :  :    | ::| :| | |  :|:: ::   |
Db     793 LVTDSAGKQLQRQLSSSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQ 849

Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
           |  |||  |::| |  ::|| |  ||| |  |   | :||| |      | |      |
Db     850 VKLSVYWDYMKAIGLFISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTK 905

Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
           |  |:      :    :::  |||| :            | : ||  || :|   ||||||
Db     906 VRLSVYGALGISQGIAVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPM 953

Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
           ||: ||:| ::|||||::| ||  :|   :||: ::  |     :|    |   : : |
Db     954 SFFERTPSGNLVNRFSKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPP 1013

Qy    1021 LVILFSVLHIVSRVLI---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRY 1077
           | :::     | |  :   |:||||:::::|| ||   :: |:: | |: : : |:|:
Db    1014 LGLIY---FFVQRFYVASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQS 1070

Qy    1078 QELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAV 1137
             :|:||  ::    | |||||||: :   ::    |  |:    :     ||::||::
Db    1071 DLKVDENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSL 1130

Qy    1138 QLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFEN 1197
           |:|    : ||::|| |    :|||:  | :|   ||| :|:  ||   ||| | | | |
Db    1131 QVTTYLNWLVRMSSEMETNIVAVERLKEYSET-EKEAPWQIQETAPPSSWPQVGRVEFRN 1189

Qy    1198 AEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVR 1257
             :||||:|  ||: :: ||   ||:|||||||:|||| : |||: | : | | |||:
Db    1190 YCLRYREDLDFVLRHINVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGIN 1249

Qy    1258 ISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPL 1317
           |: ||| ||| |::||||:|||||::| |||||:||:::::| :||  |:|: :: ||
Db    1250 IAKIGLHDLRFKITIIPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPD 1309

Qy    1318 KLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFA 1377
           ||: |  | |:| |||:|||:|:|||||  |||:|||||||:| ||| ||| |||  |
Db    1310 KLDHECAEGGENLSVGQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFE 1369

Qy    1378 DCTMLTIAHRLHTVLGSDR 1396
           |||:|||||||:|::  |
Db    1370 DCTVLTIAHRLNTIMDYTR 1388
```

```
RESULT 10
US-09-935-625-26957
; Sequence 26957, Application US/09935625
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
;  TITLE OF INVENTION:  MODULATING VARIOUS RESPONSES
;  FILE REFERENCE: 2750-1481P
;  CURRENT APPLICATION NUMBER: US/09/935,625
;  CURRENT FILING DATE:  2001-08-24
;  NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26957
;   LENGTH: 1510
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: 1..1510
;   OTHER INFORMATION: Ceres Seq. ID no. 3447801
US-09-935-625-26957
```

Query Match 27.7%; Score 2023.5; DB 5; Length 1510;
Best Local Similarity 34.4%; Pred. No. 1.2e-141;
Matches 478; Conservative 239; Mismatches 500; Indels 171; Gaps 21;

```
Qy      74 EEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDV 133
           || | |:              |  :|    | ||  : ||||: |  :  |:  |: :||
Db     105 EELPGGE-----------NICPERH----ANLFDSIFFSWLNPLMTLGSKR-PLTEKDV 147

Qy     134 WSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAG 193
           | |   : ::   |  :: | :|| :  |          |           ::  :  | |
Db     148 WHLDTWDKTETLMRSFQKSWDKELEKPKP---------W----------LLRALNNSLGG 188
```

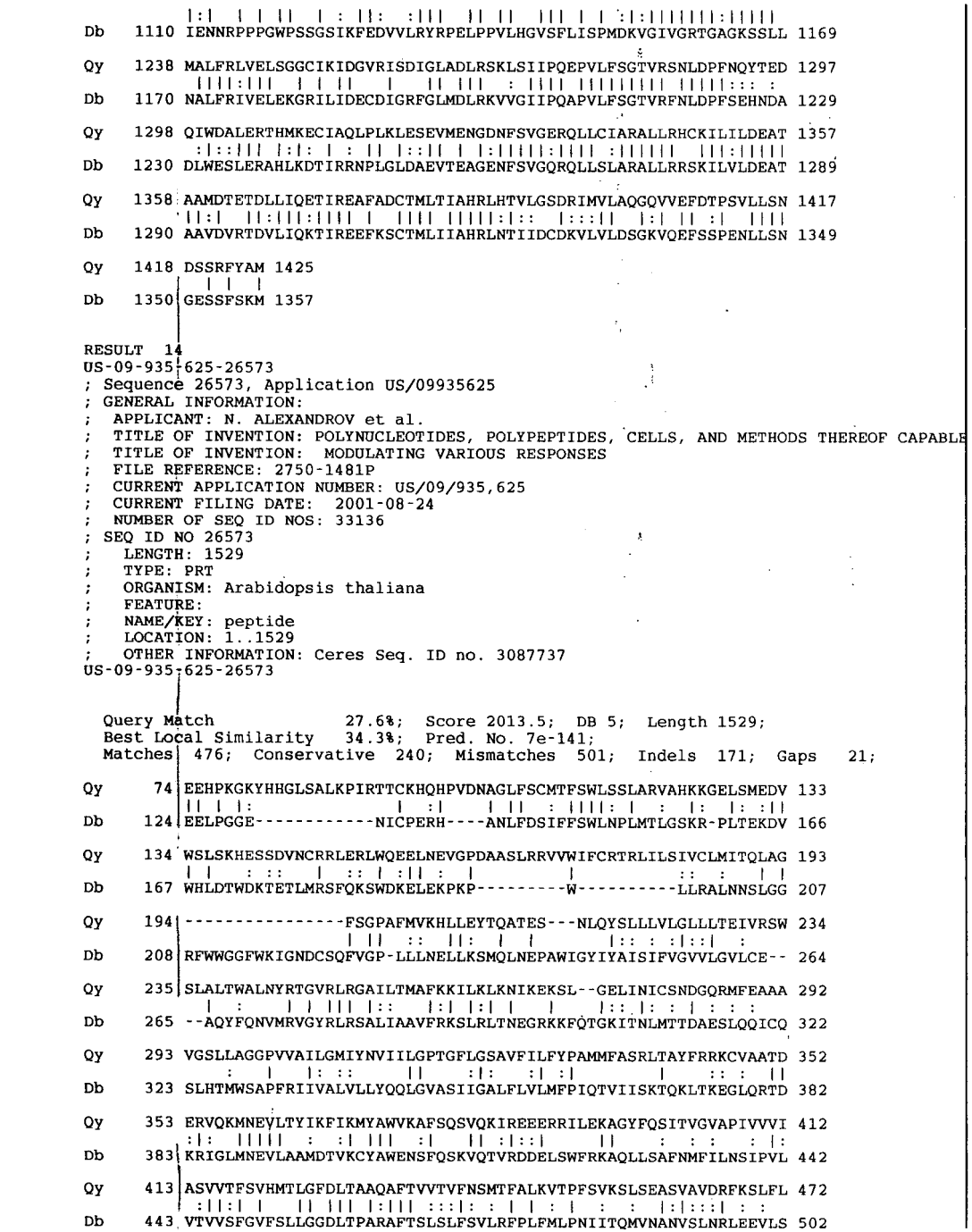
```
Qy    194 ----------------FSGPAFMVKHLLEYTQATES---NLQYSLLLVLGLLLTEIVRSW 234
Db    189 RFWWGGFWKIGNDCSQFVGP-LLLNELLKSMQLNEPAWIGYIYAISIFVGVVLGVLCE-- 245

Qy    235 SLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSL--GELINICSNDGQRMFEAAA 292
Db    246 --AQYFQNVMRVGYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQ 303

Qy    293 VGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATD 352
Db    304 SLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQTVIISKTQKLTKEGLQRTD 363

Qy    353 ERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVI 412
Db    364 KRIGLMNEVLAAMDTVKCYAWENSFQSKVQTVRDDELSWFRKAQLLSAFNMFILNSIPVL 423

Qy    413 ASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFL 472
Db    424 VTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPLFMLPNIITQMVNANVSLNRLEEVLS 483

Qy    473 MEEVHMIKNKPASP-HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVR 531
Db    484 TEERVLLPNPPIEPGQPAISIRNGYFSWDS------------------------------ 513

Qy    532 QLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLV 591
Db    514 --------------------KADRP------------------TLSNINLDIPLGSLV 533

Qy    592 GICGSVGSGKTSLISAILGQM-TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYD 650
Db    534 AVVGSTGEGKTSLISAMLGELPARSDATVTLRGSVAYVPQVSWIFNATVRDNILFGAPFD 593

Qy    651 EERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDD 710
Db    594 QEKYERVIDVTALQHDLELLPGGDLTEIGERGVNISGGQKQRVSMARAVYSNSDVCILDD 653

Qy    711 PLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db    654 PLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQVDKILLVHEGTVKEEGTYEEL 713

Qy    771 MNLNGDYATIFNNL--------LLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKA 822
Db    714 CHSGPLFQRLMENAGKVEDYSEENGEAEVDQTSVKPVENGNANNLQKDGIETKNSKEGNS 773

Qy    823 VKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSY 882
Db    774 V------LVKREERETGVVSWKVLERYQNALGGAWVVMMLVICYVLTQVFRVSSSTWLSE 827

Qy    883 WIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLR 942
Db    828 WTDSG---TPKTHG--------------PLFYNIVYALLSFGQVSVTLINSYWLIMSSLY 870

Qy    943 ASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFF 1002
Db    871 AAKKMHDAMLGSILRAPMVFFQTNPLGRIINRFAKDMGDIDRTVAVFVNMFMGSIAQLLS 930

Qy   1003 CVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLA 1062
Db    931 TVILIGIVSTLSLWAIMPLLVVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLS 990

Qy   1063 TIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHG 1122
Db    991 SIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVLGGLMVWLTASLAVMQNG 1050

Qy   1123 QI--PPAYA---GLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPAR 1177
Db   1051 KAANQQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNYIEIPS-EAPLV 1109

Qy   1178 IKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLG 1237
Db   1110 IENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSFLISPMDKVGIVGRTGAGKSSLL 1169

Qy   1238 MALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTED 1297
Db   1170 NALFRIVELEKGRILIDECDIGRFGLMDLRKVLGIIPQAPVLFSGTVRFNLDPFSEHNDA 1229

Qy   1298 QIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEAT 1357
Db   1230 DLWESLERAHLKDTIRRNPLGLDAEVTEAGENFSVGQRQLLSLARALLRRSKILVLDEAT 1289

Qy   1358 AAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSN 1417
Db   1290 AAVDVRTDVLIQKTIREEFKSCTMLIIAHRLNTIIDCDKVLVLDSGKVQEFSSPENLLSN 1349

Qy   1418 DSSRFYAM 1425
Db   1350 GESSFSKM 1357
```

RESULT 11
US-09-935-625-26956
; Sequence 26956, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26956
;   LENGTH: 1529
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: 1..1529
;   OTHER INFORMATION: Ceres Seq. ID no. 3447800
US-09-935-625-26956

```
  Query Match             27.7%;  Score 2023.5;  DB 5;  Length 1529;
  Best Local Similarity   34.4%;  Pred. No. 1.2e-141;
  Matches  478;  Conservative  239;  Mismatches  500;  Indels  171;  Gaps   21;

Qy     74 EEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDV 133
Db    124 EELPGGE------------NICPERH----ANLFDSIFFSWLNPLMTLGSKR-PLTEKDV 166

Qy    134 WSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAG 193
Db    167 WHLDTWDKTETLMRSFQKSWDKELEKPKP---------W----------LLRALNNSLGG 207

Qy    194 ----------------FSGPAFMVKHLLEYTQATES---NLQYSLLLVLGLLLTEIVRSW 234
Db    208 RFWWGGFWKIGNDCSQFVGP-LLLNELLKSMQLNEPAWIGYIYAISIFVGVVLGVLCE-- 264

Qy    235 SLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSL--GELINICSNDGQRMFEAAA 292
Db    265 --AQYFQNVMRVGYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQ 322

Qy    293 VGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATD 352
Db    323 SLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQTVIISKTQKLTKEGLQRTD 382

Qy    353 ERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVI 412
Db    383 KRIGLMNEVLAAMDTVKCYAWENSFQSKVQTVRDDELSWFRKAQLLSAFNMFILNSIPVL 442

Qy    413 ASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFL 472
Db    443 VTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPLFMLPNIITQMVNANVSLNRLEEVLS 502

Qy    473 MEEVHMIKNKPASP-HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVR 531
Db    503 TEERVLLPNPPIEPGQPAISIRNGYFSWDS------------------------------ 532
```

```
Qy    532 QLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLV 591
                                  :||                   || :|:|:|  | ||
Db    533 ---------------------KADRP-------------------TLSNINLDIPLGSLV 552

Qy    592 GICGSVGSGKTSLISAILGQM-TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYD 650
           : || | ||||||||:||::    : :: : |: ||| | :|| |||:|||||||  :|
Db    553 AVVGSTGEGKTSLISAMLGELPARSDATVTLRGSVAYVPQVSWIFNATVRDNILFGAPFD 612

Qy    651 EERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDD 710
          :|:|  |::   |: || :||  |||||||| |:||||:||:|:|||:||:  :-||||
Db    613 QEKYERVIDVTALQHDLELLPGGDLTEIGERGVNISGGQKQRVSMARAVYSNSDVCILDD 672

Qy    711 PLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
          |||||||||   :|    |:: |    | : ||:|| :|    |::: : || : | ||:|||
Db    673 PLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQVDKILLVHEGTVKEEGTYEEL 732

Qy    771 MNLNGDYATIFNNL--------LLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKA 822
           :     :  |          ||        : : |    :|:  |  | :| : |:  :
Db    733 CHSGPLFQRLMENAGKVEDYSEENGEAEVDQTSVKPVENGNANNLQKDGIETKNSKEGNS 792

Qy    823 VKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSY 882
          |        ||: ||:  | | | |   |  | ||     :::: ::|      |: |||
Db    793 V------LVKREERETGVVSWKVLERYQNALGGAWVVMMLVICYVLTQVFRVSSSTWLSE 846

Qy    883 WIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLR 942
          |   |   |  | |                     :| :||| :  : |     :  :|
Db    847 WTDSG---TPKTHG--------------PLFYNIVYALLSFGQVSVTLINSYWLIMSSLY 889

Qy    943 ASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFF 1002
          |: ::|| :    |||:|| || | | |||:|||:||| ::|  :    :  ||: ::  :
Db    890 AAKKMHDAMLGSILRAPMVFFQTNPLGRIINRFAKDMGDIDRTVAVFVNMFMGSIAQLLS 949

Qy   1003 CVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLA 1062
           |  :|  |      | : ||:::|     ::  :    ||:||:|: :|:|   :  :|: ||:
Db    950 TVILIGIVSTLSLWAIMPLLVVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLS 1009

Qy   1063 TIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHG 1122
          :| ||                 :|:|    :    |  ||| :||:::  ::   | :: |: :|
Db   1010 SIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVLGGLMVWLTASLAVMQNG 1069

Qy   1123 QI--PPAYA---GLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPAR 1177
          :     |||    || :|||: :|         :||||  |       ||||:  :||:  | |||
Db   1070 KAANQQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNYIEIPS-EAPLV 1128

Qy   1178 IKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLG 1237
          |:|  | | ||   | : ||:  :|||  || ||  |||  | | |:|||||||||:|||||
Db   1129 IENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSFLISPMDKVGIVGRTGAGKSSLL 1188

Qy   1238 MALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTED 1297
           ||||:|||  | | ||    |   || |||  |  ||||  ||||||||| ||||||::: :
Db   1189 NALFRIVELEKGRILIDECDIGRFGLMDLRKVLGIIPQAPVLFSGTVRFNLDPFSEHNDA 1248

Qy   1298 QIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEAT 1357
           :|::|||  |:|: | : || |:|:|  :  ||: ||||||||  :|||||   |||:||||
Db   1249 DLWESLERAHLKDTIRRNPLGLDAEVTEAGENFSVGQRQLLSLARALLRRSKILVLDEAT 1308

Qy   1358 AAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSN 1417
          ||:|  ||:||:||||| |  ||||  ||||:||::  |:::||:  |:| || :| ||||
Db   1309 AAVDVRTDVLIQKTIREEFKSCTMLIIAHRLNTIIDCDKVLVLDSGKVQEFSSPENLLSN 1368

Qy   1418 DSSRFYAM 1425
            | | |
Db   1369 GESSFSKM 1376

RESULT 12
US-09-935-625-26955
; Sequence 26955, Application US/09935625
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
;  TITLE OF INVENTION:  MODULATING VARIOUS RESPONSES
;  FILE REFERENCE: 2750-1481P
;  CURRENT APPLICATION NUMBER: US/09/935,625
;  CURRENT FILING DATE:  2001-08-24
;  NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26955
;   LENGTH: 1622
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: 1..1622
;   OTHER INFORMATION: Ceres Seq. ID no. 3447799
US-09-935-625-26955

  Query Match             27.7%;  Score 2023.5;  DB 5;  Length 1622;
  Best Local Similarity   34.4%;  Pred. No. 1.4e-141;
  Matches  478;  Conservative  239;  Mismatches  500;  Indels  171;  Gaps   21;

Qy     74 EEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDV 133
          || | |:                |  :|    | ||  : ||||: |   :  |:  |: :||
Db    217 EELPGGE-----------NICPERH----ANLFDSIFFSWLNPLMTLGSKR-PLTEKDV 259

Qy    134 WSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAG 193
          | |   : ::   |  :: | :|| :  |            |             :: :  | |
Db    260 WHLDTWDKTETLMRSFQKSWDKELEKPKP---------W----------LLRALNNSLGG 300

Qy    194 ----------------FSGPAFMVKHLLEYTQATES---NLQYSLLLVLGLLLTEIVRSW 234
                          | ||  ::  ||:  |   |       |:: : :|::|  :
Db    301 RFWWGGFWKIGNDCSQFVGP-LLLNELLKSMQLNEPAWIGYIYAISIFVGVVLGVLCE-- 357

Qy    235 SLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSL--GELINICSNDGQRMFEAAA 292
            |  :   | | ||| |::   |:| |:| |   |     |:: |: : | : : :
Db    358 --AQYFQNVMRVGYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQ 415

Qy    293 VGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATD 352
              :    |   |: ::      ||      :|:    :| :|           |    :: :  ||
Db    416 SLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQTVIISKTQKLTKEGLQRTD 475

Qy    353 ERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVI 412
          :|:  |||||   :  :| |||   :|    || :|::|      ||       :   :   : |:
Db    476 KRIGLMNEVLAAMDTVKCYAWENSFQSKVQTVRDDELSWFRKAQLLSAFNMFILNSIPVL 535

Qy    413 ASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFL 472
           :||:|   |  ||| |||  |:|:||  ::|:|:  | | |  :  |  :  | |:|::|  : :
Db    536 VTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPLFMLPNIITQMVNANVSLNRLEEVLS 595

Qy    473 MEEVHMIKNKPASP-HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVR 531
           || :: | |  |     | ::|  :|||
Db    596 TEERVLLPNPPIEPGQPAISIRNGYFSWDS----------------------------- 625

Qy    532 QLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLV 591
                                  :||                   || :|:|:|  | ||
Db    626 ---------------------KADRP-------------------TLSNINLDIPLGSLV 645

Qy    592 GICGSVGSGKTSLISAILGQM-TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYD 650
           : || | ||||||||:||::    : :: : |: ||| | :|| |||:|||||||  :|
Db    646 AVVGSTGEGKTSLISAMLGELPARSDATVTLRGSVAYVPQVSWIFNATVRDNILFGAPFD 705

Qy    651 EERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDD 710
          :|:|  |::   |: || :||  |||||||| |:||||:||:|:|||:||:  : ||||
Db    706 QEKYERVIDVTALQHDLELLPGGDLTEIGERGVNISGGQKQRVSMARAVYSNSDVCILDD 765

Qy    711 PLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
          |||||||||   :|    |:: |    | : ||:|| :|    |::: : || : | ||:|||
Db    766 PLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQVDKILLVHEGTVKEEGTYEEL 825

Qy    771 MNLNGDYATIFNNL--------LLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKA 822
           :     :  |          ||        : : |    :|:  |  | :| : |:  :
Db    826 CHSGPLFQRLMENAGKVEDYSEENGEAEVDQTSVKPVENGNANNLQKDGIETKNSKEGNS 885

Qy    823 VKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSY 882
          |        ||: ||:  | | | |   |  | ||     :::: ::|      |: |||
```

```
Db     886 V------LVKREEERETGVVSWKVLERYQNALGGAWVVMMLVICYVLTQVFRVSSSTWLSE 939

Qy     883 WIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLR 942

Db     940 WTDSG---TPKTHG-------------PLFYNIVYALLSFGQVSVTLINSYWLIMSSLY 982

Qy     943 ASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFF 1002

Db     983 AAKKMHDAMLGSILRAPMVFFQTNPLGRIINRFAKDMGDIDRTVAVFVNMFMGSIAQLLS 1042

Qy    1003 CVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLA 1062

Db    1043 TVILIGIVSTLSLWAIMPLLVVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLS 1102

Qy    1063 TIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHG 1122

Db    1103 SIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVLGGLMVWLTASLAVMQNG 1162

Qy    1123 QI--PPAYA---GLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPAR 1177

Db    1163 KAANQQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNYIEIPS-EAPLV 1221

Qy    1178 IKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLG 1237

Db    1222 IENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSFLISPMDKVGIVGRTGAGKSSLL 1281

Qy    1238 MALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTED 1297

Db    1282 NALFRIVELEKGRILIDECDIGRFGLMDLRKVLGIIPQAPVLFSGTVRFNLDPFSEHNDA 1341

Qy    1298 QIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEAT 1357

Db    1342 DLWESLERAHLKDTIRRNPLGLDAEVTEAGENFSVGQRQLLSLARALLRRSKILVLDEAT 1401

Qy    1358 AAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSN 1417

Db    1402 AAVDVRTDVLIQKTIREEFKSCTMLIIAHRLNTIIDCDKVLVLDSGKVQEFSSPENLLSN 1461

Qy    1418 DSSRFYAM 1425

Db    1462 GESSFSKM 1469


RESULT 13
US-09-935-625-26574
; Sequence 26574, Application US/09935625
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
;  TITLE OF INVENTION:  MODULATING VARIOUS RESPONSES
;  FILE REFERENCE: 2750-1481P
;  CURRENT APPLICATION NUMBER: US/09/935,625
;  CURRENT FILING DATE:  2001-08-24
;  NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26574
;   LENGTH: 1510
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: 1..1510
;   OTHER INFORMATION: Ceres Seq. ID no. 3087738
US-09-935-625-26574


  Query Match           27.6%;  Score 2013.5;  DB 5;  Length 1510;
  Best Local Similarity   34.3%;  Pred. No. 6.8e-141;
  Matches  476;  Conservative  240;  Mismatches  501;  Indels  171;  Gaps   21;

Qy      74 EEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDV 133

Db     105 EELPGGE------------NICPERH----ANLFDSIFFSWLNPLMTLGSKR-PLTEKDV 147

Qy     134 WSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAG 193

Db     148 WHLDTWDKTETLMRSFQKSWDKELEKPKP---------W----------LLRALNNSLGG 188

Qy     194 ----------------FSGPAFMVKHLLEYTQATES---NLQYSLLLVLGLLLTEIVRSW 234

Db     189 RFWWGGFWKIGNDCSQFVGP-LLLNELLKSMQLNEPAWIGYIYAISIFVGVVLGVLCE-- 245

Qy     235 SLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSL--GELINICSNDGQRMFEAAA 292

Db     246 --AQYFQNVMRVGYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQ 303

Qy     293 VGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATD 352

Db     304 SLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQTVIISKTQKLTKEGLQRTD 363

Qy     353 ERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVI 412

Db     364 KRIGLMNEVLAAMDTVKCYAWENSFQSKVQTVRDDELSWFRKAQLLSAFNMFILNSIPVL 423

Qy     413 ASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFL 472

Db     424 VTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPLFMLPNIITQMVNANVSLNRLEEVLS 483

Qy     473 MEEVHMIKNKPASP-HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVR 531

Db     484 TEERVLLPNPPIEPGQPAISIRNGYFSWDS---------------------------- 513

Qy     532 QLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLV 591

Db     514 --------------------KADRP------------------TLSNINLDIPLGSLV 533

Qy     592 GICGSVGSGKTSLISAILGQM-TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYD 650

Db     534 AVVGSTGEGKTSLISAMLGELPARSDATVTLRGSVAYVPQVSWIFNATVRDNILFGAPFD 593

Qy     651 EERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDD 710

Db     594 QEKYERVIDVTALQHDLELLPGGDLTEIGERGVNISGGQKQRVSMARAVYSNSDVCILDE 653

Qy     711 PLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770

Db     654 PLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQVDKILLVHEGTVKEEGTYEEL 713

Qy     771 MNLNGDYATIFNNL--------LLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKA 822

Db     714 CHSGPLFPRLMENAGKVEDYSEENGEAEVHQTSVKPVENGNANNLQKDGIETKNSKEGNS 773

Qy     823 VKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSY 882

Db     774 V------LVKREERETGVVSWKVLERYQNALGGAWVVMMLVICYVLTQVFRVSSITWLSE 827

Qy     883 WIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLR 942

Db     828 WTDSG---TPKTHG-------------PLFYNIVYALLSFGQVSVTLINSYWLIMSSLY 870

Qy     943 ASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFF 1002

Db     871 AAKKMHDAMLGSILRAPMVFFQTNPLGRIINRFAKDMGDIDRTVAVFVNMFMGSIAQLLS 930

Qy    1003 CVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLA 1062

Db     931 TVILIGIVSTLSLWAIMPLLVVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLS 990

Qy    1063 TIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHG 1122

Db     991 SIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVLGGLMVWWTASLAVMQNG 1050

Qy    1123 QI--PPAYA---GLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPAR 1177

Db    1051 KAANQQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNYIEIPS-EAPLV 1109

Qy    1178 IKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLG 1237
```


Db 1110 IENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSFLISPMDKVGIVGRTGAGKSSLL 1169
Qy 1238 MALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTED 1297
Db 1170 NALFRIVELEKGRILIDECDIGRFGLMDLRKVVGIIPQAPVLFSGTVRFNLDPFSEHNDA 1229
Qy 1298 QIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEAT 1357
Db 1230 DLWESLERAHLKDTIRRNPLGLDAEVTEAGENFSVGQRQLLSLARALLRRSKILVLDEAT 1289
Qy 1358 AAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSN 1417
Db 1290 AAVDVRTDVLIQKTIREEFKSCTMLIIAHRLNTIIDCDKVLVLDSGKVQEFSSPENLLSN 1349
Qy 1418 DSSRFYAM 1425
Db 1350 GESSFSKM 1357
RESULT 14
US-09-935-625-26573
; Sequence 26573, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26573
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..1529
; OTHER INFORMATION: Ceres Seq. ID no. 3087737
US-09-935-625-26573
Query Match 27.6%; Score 2013.5; DB 5; Length 1529;
Best Local Similarity 34.3%; Pred. No. 7e-141;
Matches 476; Conservative 240; Mismatches 501; Indels 171; Gaps 21;
Qy 74 EEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDV 133
Db 124 EELPGGE----------NICPERH----ANLFDSIFFSWLNPLMTLGSKR-PLTEKDV 166
Qy 134 WSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAG 193
Db 167 WHLDTWDKTETLMRSFQKSWDKELEKPKP---------W----------LLRALNNSLGG 207
Qy 194 ---------------FSGPAFMVKHLLEYTQATES---NLQYSLLLVLGLLLTEIVRSW 234
Db 208 RFWWGGFWKIGNDCSQFVGP-LLLNELLKSMQLNEPAWIGYIYAISIFVGVVLGVLCE-- 264
Qy 235 SLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSL--GELINICSNDGQRMFEAAA 292
Db 265 --AQYFQNVMRVGYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQ 322
Qy 293 VGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATD 352
Db 323 SLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQTVIISKTQKLTKEGLQRTD 382
Qy 353 ERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVI 412
Db 383 KRIGLMNEVLAAMDTVKCYAWENSFQSKVQTVRDDELSWFRKAQLLSAFNMFILNSIPVL 442
Qy 413 ASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFL 472
Db 443 VTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPLFMLPNIITQMVNANVSLNRLEEVLS 502
Qy 473 MEEVHMIKNKPASP-HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVR 531
Db 503 TEERVLLPNPPIEPGQPAISIRNGYFSWDS---------------------------- 532
Qy 532 QLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLV 591
Db 533 ----------------------KADRP------------------TLSNINLDIPLGSLV 552
Qy 592 GICGSVGSGKTSLISAILGQM-TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYD 650
Db 553 AVVGSTGEGKTSLISAMLGELPARSDATVTLRGSVAYVPQVSWIFNATVRDNILFGAPFD 612
Qy 651 EERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDD 710
Db 613 QEKYERVIDVTALQHDLELLPGGDLTEIGERGVNISGGQKQRVSMARAVYSNSDVCILDE 672
Qy 711 PLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db 673 PLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQVDKILLVHEGTVKEEGTYEEL 732
Qy 771 MNLNGDYATIFNNL--------LLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKA 822
Db 733 CHSGPLFPRLMENAGKVEDYSEENGEAEVHQTSVKPVENGNANNLQKDGIETKNSKEGNS 792
Qy 823 VKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSY 882
Db 793 V------LVKREERETGVVSWKVLERYQNALGGAWVVMMLVICYVLTQVFRVSSITWLSE 846
Qy 883 WIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLR 942
Db 847 WTDSG---TPKTHG--------------PLFYNIVYALLSFGQVSVTLINSYWLIMSSLY 889
Qy 943 ASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFF 1002
Db 890 AAKKMHDAMLGSILRAPMVFFQTNPLGRIINRFAKDMGDIDRTVAVFVNMFMGSIAQLLS 949
Qy 1003 CVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLA 1062
Db 950 TVILIGIVSTLSLWAIMPLLVVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLS 1009
Qy 1063 TIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHG 1122
Db 1010 SIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVLGGLMVWWTASLAVMQNG 1069
Qy 1123 QI--PPAYA---GLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPAR 1177
Db 1070 KAANQQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNYIEIPS-EAPLV 1128
Qy 1178 IKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLG 1237
Db 1129 IENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSFLISPMDKVGIVGRTGAGKSSLL 1188
Qy 1238 MALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTED 1297
Db 1189 NALFRIVELEKGRILIDECDIGRFGLMDLRKVVGIIPQAPVLFSGTVRFNLDPFSEHNDA 1248
Qy 1298 QIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEAT 1357
Db 1249 DLWESLERAHLKDTIRRNPLGLDAEVTEAGENFSVGQRQLLSLARALLRRSKILVLDEAT 1308
Qy 1358 AAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSN 1417
Db 1309 AAVDVRTDVLIQKTIREEFKSCTMLIIAHRLNTIIDCDKVLVLDSGKVQEFSSPENLLSN 1368
Qy 1418 DSSRFYAM 1425
Db 1369 GESSFSKM 1376
RESULT 15
US-09-935-625-26572
; Sequence 26572, Application US/09935625

```
; GENERAL INFORMATION:
;  APPLICANT: N. ALEXANDROV et al.
;  TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
;  TITLE OF INVENTION:  MODULATING VARIOUS RESPONSES
;  FILE REFERENCE: 2750-1481P
;  CURRENT APPLICATION NUMBER: US/09/935,625
;  CURRENT FILING DATE:  2001-08-24
;  NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 26572
;   LENGTH: 1622
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: 1..1622
;   OTHER INFORMATION: Ceres Seq. ID no. 3087736
US-09-935-625-26572
```

Query Match 27.6%; Score 2013.5; DB 5; Length 1622;
Best Local Similarity 34.3%; Pred. No. 7.6e-141;
Matches 476; Conservative 240; Mismatches 501; Indels 171; Gaps 21;

```
Qy      74 EEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDV 133
           ||  | |:                |  :|    | ||  : ||||: |  :  |:  |: :||
Db     217 EELPGGE-----------NICPERH----ANLFDSIFFSWLNPLMTLGSKR-PLTEKDV 259

Qy     134 WSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAG 193
           | |   : ::   |  :: | :|| :  |          |          ::  :   | |
Db     260 WHLDTWDKTETLMRSFQKSWDKELEKPKP---------W----------LLRALNNSLGG 300

Qy     194 ----------------FSGPAFMVKHLLEYTQATES---NLQYSLLLVLGLLLTEIVRSW 234
                           | ||  ::  ||:  |  |       |:: : :|::|  :
Db     301 RFWWGGFWKIGNDCSQFVGP-LLLNELLKSMQLNEPAWIGYIYAISIFVGVVLGVLCE-- 357

Qy     235 SLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSL--GELINICSNDGQRMFEAAA 292
             |  :    | | |||  |::   |:| |:| |    |    |:: |: : | : : :
Db     358 --AQYFQNVMRVGYRLRSALIAAVFRKSLRLTNEGRKKFQTGKITNLMTTDAESLQQICQ 415

Qy     293 VGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATD 352
           :   |   |: ::     ||    :|:   :| :|      |    :: :  ||
Db     416 SLHTMWSAPFRIIVALVLLYQQLGVASIIGALFLVLMFPIQTVIISKTQKLTKEGLQRTD 475

Qy     353 ERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVI 412
           :|:  ||||  :  :| ||| :|   || :|::|     ||    :  : :   : |:
Db     476 KRIGLMNEVLAAMDTVKCYAWENSFQSKVQTVRDDELSWFRKAQLLSAFNMFILNSIPVL 535

Qy     413 ASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFL 472
           :||:| |   || ||| |:||| :::|: : | | : |  :  :  |:|:::| : :
Db     536 VTVVSFGVFSLLGGDLTPARAFTSLSLFSVLRFPLFMLPNIITQMVNANVSLNRLEEVLS 595

Qy     473 MEEVHMIKNKPASP-HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVR 531
           ||  :: | |  |    | ::|   :|||
Db     596 TEERVLLPNPPIEPGQPAISIRNGYFSWDS---------------------------- 625

Qy     532 QLQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLV 591
                              :||                  || :|:|:|  | ||
Db     626 ---------------------KADRP------------------TLSNINLDIPLGSLV 645

Qy     592 GICGSVGSGKTSLISAILGQM-TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYD 650
           : || | ||||||||:||::    : :: : |: ||| | :|| |||:|||||  :|
Db     646 AVVGSTGEGKTSLISAMLGELPARSDATVTLRGSVAYVPQVSWIFNATVRDNILFGAPFD 705

Qy     651 EERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDD 710
           :|:|  |::   |: || :||  |||||||||  |:||||:||:|:|||:||:  : |||:
Db     706 QEKYERVIDVTALQHDLELLPGGDLTEIGERGVNISGGQKQRVSMARAVYSNSDVCILDE 765

Qy     711 PLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
           ||||||||||  :|   |:: |   | : ||:|| :|   |::: : || : | ||:|||
Db     766 PLSALDAHVGQQVFEKCIKRELGQTTRVLVTNQLHFLSQVDKILLVHEGTVKEEGTYEEL 825

Qy     771 MNLNGDYATIFNNL--------LLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKA 822
           :   :  :  |           ||    : : |   :|:    |  | :| : |:  :
```

```
Db     826 CHSGPLFPRLMENAGKVEDYSEENGEAEVHQTSVKPVENGNANNLQKDGIETKNSKEGNS 885

Qy     823 VKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSY 882
           |      ||: ||:  | | | |   |  | ||    ::::  ::|       |  |||
Db     886 V------LVKREERETGVVSWKVLERYQNALGGAWVVMMLVICYVLTQVFRVSSITWLSE 939

Qy     883 WIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLR 942
           |   |   | | |                :|  :|||     : :  |     :  :|
Db     940 WTDSG---TPKTHG--------------PLFYNIVYALLSFGQVSVTLINSYWLIMSSLY 982

Qy     943 ASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFF 1002
           |: ::|| :   |||:|| || | | |||:|||:||| ::|  :     ||: ::  :
Db     983 AAKKMHDAMLGSILRAPMVFFQTNPLGRIINRFAKDMGDIDRTVAVFVNMFMGSIAQLLS 1042

Qy    1003 CVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLA 1062
           | :|  |    | |: ||:::|   ::  :   ||:||:|: |:||  :    :: ||:
Db    1043 TVILIGIVSTLSLWAIMPLLVVFYGAYLYYQNTSREIKRMDSTTRSPVYAQFGEALNGLS 1102

Qy    1063 TIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHG 1122
           :| ||            :|:|     :   | ||| :||:::   ::  |  : |: :|
Db    1103 SIRAYKAYDRMAEINGRSMDNNIRFTLVNMAANRWLGIRLEVLGGLMVWWTASLAVMQNG 1162

Qy    1123 QI--PPAYA---GLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPAR 1177
           :    |||   || :|||: :|      :|||| |    ||||: :||:  | |||
Db    1163 KAANQQAYASTMGLLLSYALSITSSLTAVLRLASLAENSLNSVERVGNYIEIPS-EAPLV 1221

Qy    1178 IKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLG 1237
           |:|  | | ||  | : ||:  :|||  || ||  ||| | | :|:|||||||:|||||
Db    1222 IENNRPPPGWPSSGSIKFEDVVLRYRPELPPVLHGVSFLISPMDKVGIVGRTGAGKSSLL 1281

Qy    1238 MALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTED 1297
           ||||:|||  | | ||   |   || |||  : |||| |||||||| ||||| ::: :
Db    1282 NALFRIVELEKGRILIDECDIGRFGLMDLRKVVGIIPQAPVLFSGTVRFNLDPFSEHNDA 1341

Qy    1298 QIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEAT 1357
           :|::||| |:|: | : || |::|| | |:|||||:|||| :||||||  |||:|||||
Db    1342 DLWESLERAHLKDTIRRNPLGLDAEVTEAGENFSVGQRQLLSLARALLRRSKILVLDEAT 1401

Qy    1358 AAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSN 1417
           ||:|  ||:|||:|||| |  |||| |||||:|::  |:::||  |:| || :|  ||||
Db    1402 AAVDVRTDVLIQKTIREEFKSCTMLIIAHRLNTIIDCDKVLVLDSGKVQEFSSPENLLSN 1461

Qy    1418 DSSRFYAM 1425
              | |
Db    1462 GESSFSKM 1469
```

Search completed: August 11, 2002, 11:13:47
Job time: 6422 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 09:13:40 ; Search time 92.45 Seconds
(without alignments)
12878.157 Million cell updates/sec

Title: US-09-528-031-1
Perfect score: 4847
Sequence: 1 GGCTCATGCTCGGGAGCGTG.....AAAAAAAAAGGGCGGCCGC 4847

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4847	100.0	4847	3	US-09-061-400-1	Sequence 1, Appli
2	4775.4	98.5	4781	2	US-09-001-273-1	Sequence 1, Appli
3	4775.4	98.5	4781	4	US-08-843-459A-1	Sequence 1, Appli
4	511.2	10.5	5011	1	US-08-463-092B-3	Sequence 3, Appli
5	511.2	10.5	5011	2	US-08-462-109A-3	Sequence 3, Appli
6	511.2	10.5	5011	2	US-08-460-907B-3	Sequence 3, Appli
7	511.2	10.5	5011	3	US-08-463-179A-3	Sequence 3, Appli
8	511.2	10.5	5011	3	US-08-461-384B-3	Sequence 3, Appli
9	506.4	10.4	5011	1	US-08-141-893-1	Sequence 1, Appli
10	506.4	10.4	5011	1	US-08-463-092B-1	Sequence 1, Appli
11	506.4	10.4	5011	2	US-08-462-109A-1	Sequence 1, Appli
12	506.4	10.4	5011	2	US-08-460-907B-1	Sequence 1, Appli
13	506.4	10.4	5011	3	US-08-463-179A-1	Sequence 1, Appli
14	506.4	10.4	5011	3	US-08-461-384B-1	Sequence 1, Appli
15	506.4	10.4	5011	3	US-08-407-207A-1	Sequence 1, Appli
16	435.8	9.0	6140	4	US-09-439-313-536	Sequence 536, App
17	425.4	8.8	6082	4	US-09-439-313-535	Sequence 535, App
18	420.4	8.7	5889	1	US-08-463-092B-5	Sequence 5, Appli
19	420.4	8.7	5889	2	US-08-462-109A-5	Sequence 5, Appli
20	420.4	8.7	5889	2	US-08-460-907B-5	Sequence 5, Appli
21	420.4	8.7	5889	3	US-08-463-179A-5	Sequence 5, Appli
22	420.4	8.7	5889	3	US-08-461-384B-5	Sequence 5, Appli
23	370	7.6	4931	4	US-08-726-320-2	Sequence 2, Appli
24	370	7.6	4931	4	US-09-208-716-2	Sequence 2, Appli
25	346	7.1	4877	2	US-08-404-531B-7	Sequence 7, Appli
26	346	7.1	4877	2	US-08-404-531B-8	Sequence 8, Appli
27	346	7.1	4877	3	US-08-476-900A-7	Sequence 7, Appli
28	346	7.1	4877	3	US-08-476-900A-8	Sequence 8, Appli
29	346	7.1	4877	3	US-08-488-546A-7	Sequence 7, Appli
30	346	7.1	4877	3	US-08-488-546A-8	Sequence 8, Appli
31	344.4	7.1	5175	4	US-08-972-927-4	Sequence 4, Appli
32	342.6	7.1	5110	2	US-08-404-531B-4	Sequence 4, Appli
33	342.6	7.1	5110	2	US-08-404-531B-5	Sequence 5, Appli
34	342.6	7.1	5110	3	US-08-476-900A-4	Sequence 4, Appli
35	342.6	7.1	5110	3	US-08-476-900A-5	Sequence 5, Appli
36	342.6	7.1	5110	3	US-08-488-546A-4	Sequence 4, Appli
37	342.6	7.1	5110	3	US-08-488-546A-5	Sequence 5, Appli
38	340.8	7.0	463	2	US-09-001-273-3	Sequence 3, Appli
39	340.8	7.0	463	3	US-09-061-400-3	Sequence 3, Appli
40	340.8	7.0	463	4	US-08-843-459A-3	Sequence 3, Appli
41	336.2	6.9	5232	4	US-08-972-927-1	Sequence 1, Appli
42	330.8	6.8	2454	2	US-08-404-531B-32	Sequence 32, Appl
43	330.8	6.8	2454	3	US-08-476-900A-32	Sequence 32, Appl
44	330.8	6.8	2454	3	US-08-488-546A-32	Sequence 32, Appl
45	294	6.1	2294	2	US-08-404-531B-30	Sequence 30, Appl

ALIGNMENTS

```
RESULT   1
US-09-061-400-1
; Sequence 1, Application US/09061400
; Patent No. 6077936
;  GENERAL INFORMATION:
;    APPLICANT:  SHYJAN, Andrew
;    TITLE OF INVENTION:  NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/061,400
;      FILING DATE:  16-APRIL-1998
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth A. Hanley
;      REGISTRATION NUMBER:  33,505
;      REFERENCE/DOCKET NUMBER:  MNI-056CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 742-4214
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4847 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  116..4426
US-09-061-400-1


  Query Match             100.0%;  Score 4847;  DB 3;  Length 4847;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4847;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60

Qy     61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120

Qy    121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180

Qy    181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240

Qy    241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300

Qy    301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360

Qy    361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420

Qy    421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480

Qy    481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540

Qy    541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600

Qy    601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660

Qy    661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720

Qy    721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780

Qy    781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840

Qy    841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900

Qy    901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960

Qy    961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020

Qy   1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080

Qy   1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140

Qy   1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200

Qy   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260

Qy   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320

Qy   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380

Qy   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440

Qy   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500

Qy   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560

Qy   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620

Qy   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680

Qy   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740

Qy   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800

Qy   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860

Qy   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920

Qy   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980

Qy   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040

Qy   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100

Qy   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160

Qy   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
```

```
Qy   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280

Qy   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340

Qy   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400

Qy   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460

Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520

Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580

Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640

Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700

Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760

Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820

Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880

Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940

Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000

Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060

Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120

Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420

Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480

Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540

Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600

Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660

Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720

Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780

Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840

Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900

Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960

Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020

Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080

Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440

Qy    4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500

Qy    4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560

Qy    4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620

Qy    4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680

Qy    4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740

Qy    4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800

Qy    4801 AAGCACTGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4801 AAGCACTGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
```

```
RESULT   2
US-09-001-273-1
; Sequence 1, Application US/09001273
; Patent No. 5994130
;  GENERAL INFORMATION:
;    APPLICANT:  SHYJAN, Andrew
;    TITLE OF INVENTION:  NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/001,273
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FENTON, Gillian M
;      REGISTRATION NUMBER:  36,508
;      REFERENCE/DOCKET NUMBER:  MIL-001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4781 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..4360
US-09-001-273-1
```

```
  Query Match             98.5%;  Score 4775.4;  DB 2;  Length 4781;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4773;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      67 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT 60

Qy     127 CGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAAC 120

Qy     187 CAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 180

Qy     247 GGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTC 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTC 240

Qy     307 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 300

Qy     367 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGACAATGC 426
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     301 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGCACCCAGTGGACAATGC 360

Qy     427 TGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAA 420

Qy     487 GAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTCTGACGT 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTCTGACGT 480

Qy     547 GAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGC 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGC 540

Qy     607 TGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGT 600

Qy     667 GTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 660

Qy     727 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGG 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGG 720

Qy     787 CCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTA 780

Qy     847 CCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAA 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAA 840

Qy     907 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGG 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGG 900

Qy     967 GCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGC 960

Qy    1027 CATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC 1020
```

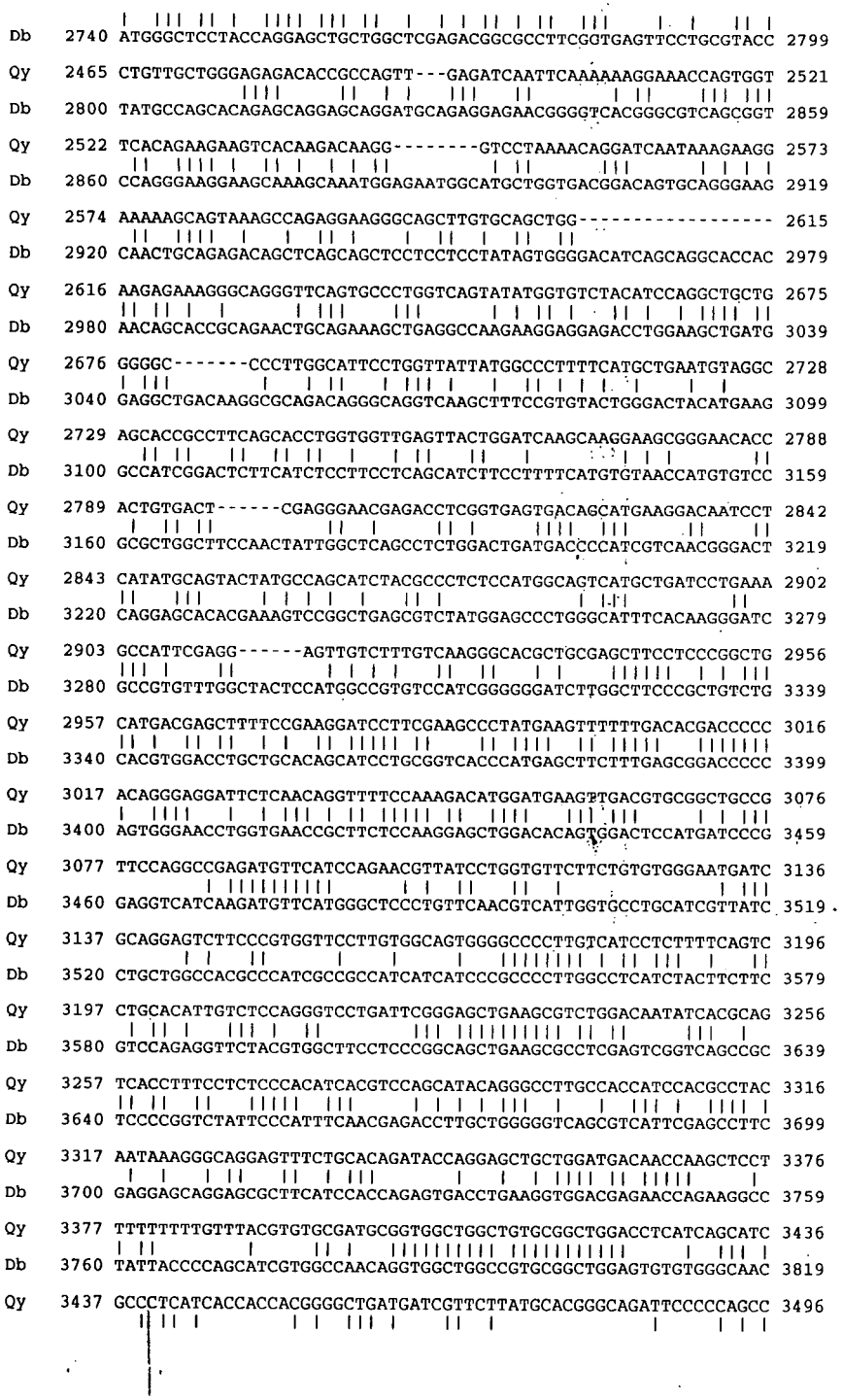
```
Qy   1087 TGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAG 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAG 1080

Qy   1147 GAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTA 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTA 1140

Qy   1207 CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAAT 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAAT 1200

Qy   1267 CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1260

Qy   1327 TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT 1320

Qy   1387 GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC 1380

Qy   1447 TTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT 1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT 1440

Qy   1507 TGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGC 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGC 1500

Qy   1567 CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC 1626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC 1560

Qy   1627 CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG 1620

Qy   1687 GGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA 1680

Qy   1747 GCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG 1740

Qy   1807 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1800

Qy   1867 GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT 1860

Qy   1927 CATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC 1920

Qy   1987 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 1980

Qy   2047 GTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAG 2040

Qy   2107 GCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAA 2100

Qy   2167 CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAG 2160

Qy   2227 CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTT 2220

Qy   2287 CAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTT 2280

Qy   2347 ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG 2340

Qy   2407 AGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCT 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCT 2400

Qy   2467 GTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACA 2460

Qy   2527 GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAA 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAA 2520

Qy   2587 GCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC 2580

Qy   2647 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGC 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGC 2640

Qy   2707 CCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGAT 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGAT 2700

Qy   2767 CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAG 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAG 2760

Qy   2827 CATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGT 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGT 2820

Qy   2887 CATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 2880

Qy   2947 CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 3006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 2940

Qy   3007 CACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 3000

Qy   3067 GCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 3126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 3060

Qy   3127 GGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCT 3186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCT 3120

Qy   3187 CTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3180

Qy   3247 TATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 3306
```

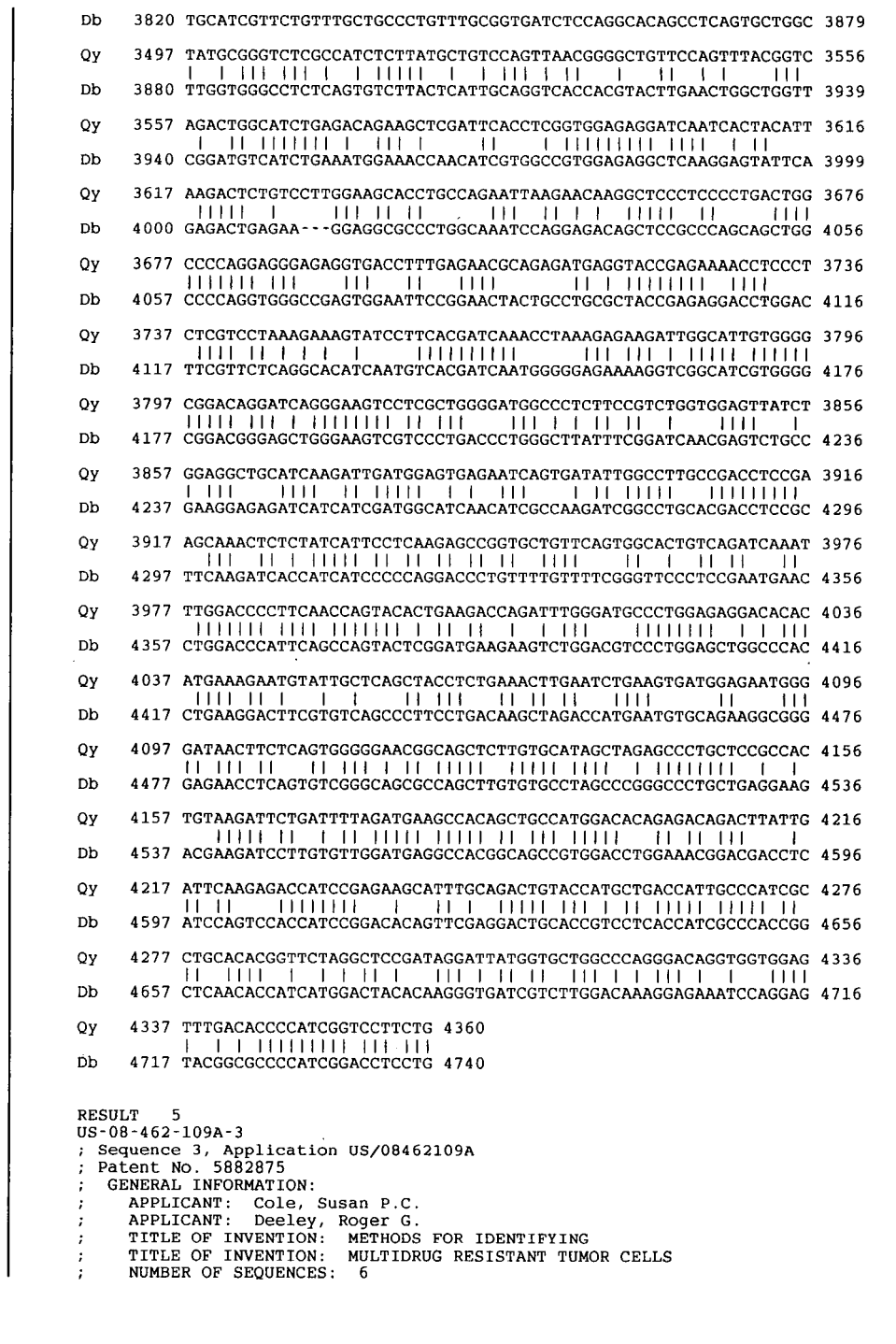
```
Db   3181 TATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 3240

Qy   3307 CCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 3366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 3300

Qy   3367 CCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCT 3426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 CCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCT 3360

Qy   3427 CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGAT 3486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGAT 3420

Qy   3487 TCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA 3546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA 3480

Qy   3547 GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA 3606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA 3540

Qy   3607 TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC 3666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC 3600

Qy   3667 CCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 3726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 3660

Qy   3727 AAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 AAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3720

Qy   3787 CATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3780

Qy   3847 GGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3840

Qy   3907 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT 3966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT 3900

Qy   3967 CAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGA 4026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGA 3960

Qy   4027 GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 4086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 4020

Qy   4087 GGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4080

Qy   4147 GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4140

Qy   4207 AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT 4266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT 4200

Qy   4267 TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACA 4326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACA 4260

Qy   4327 GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC 4386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   4261 GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC 4320

Qy   4387 CATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGA 4446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGA 4380

Qy   4447 AGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCC 4506
          |||||||||||||||||||||||::: ::|:||||||||||||||||||||||||||||
Db   4381 AGTCTCTTTTCTTTAGAGCATTGCCMYKGMMTKCCTGGGGCGGGCCCCTTCATCGCGTCC 4440

Qy   4507 TCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 TCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4500

Qy   4567 GTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGT 4626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 GTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGT 4560

Qy   4627 AAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTAT 4686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTAT 4620

Qy   4687 AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCT 4746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCT 4680

Qy   4747 GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4740

Qy   4807 TGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
          |||||||||||||||||||||||||||||||||||||||||||
Db   4741 TGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4781


RESULT   3
US-08-843-459A-1
; Sequence 1, Application US/08843459A
; Patent No. 6162616
;  GENERAL INFORMATION:
;    APPLICANT:  SHYJAN, Andrew
;    TITLE OF INVENTION:  NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/843,459A
;      FILING DATE:  16-APR-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanley, Elizabeth A.
;      REGISTRATION NUMBER:  33,505
;      REFERENCE/DOCKET NUMBER:  MNI-056 (formerly MIL-001)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4781 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  2..4360
US-08-843-459A-1

  Query Match             98.5%;  Score 4775.4;  DB 4;  Length 4781;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4773;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      67 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT  60

Qy     127 CGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAAC 120

Qy     187 CAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 180

Qy     247 GGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTC 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTC 240

Qy     307 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 300

Qy     367 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGACAATGC 426
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     301 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGCACCCAGTGGACAATGC 360

Qy     427 TGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAA 420

Qy     487 GAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGGACGAGTCTTCTGACGT 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTCTGACGT 480

Qy     547 GAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGC 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGC 540

Qy     607 TGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGT 600

Qy     667 GTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 660

Qy     727 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGG 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGG 720

Qy     787 CCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTA 780

Qy     847 CCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAA 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAA 840

Qy     907 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGG 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGG 900

Qy     967 GCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGC 960

Qy    1027 CATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC 1020

Qy    1087 TGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAG 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAG 1080

Qy    1147 GAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTA 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTA 1140

Qy    1207 CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAAT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAAT 1200

Qy    1267 CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1260

Qy    1327 TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT 1320

Qy    1387 GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC 1380

Qy    1447 TTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT 1440

Qy    1507 TGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGC 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGC 1500

Qy    1567 CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC 1560

Qy    1627 CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG 1620

Qy    1687 GGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA 1680

Qy    1747 GCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG 1740

Qy    1807 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1800

Qy    1867 GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT 1860

Qy    1927 CATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC 1920

Qy    1987 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 2046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 1980

Qy    2047 GTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAG 2106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 GTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAG 2040
```

```
Qy   2107 GCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAA 2100

Qy   2167 CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAG 2160

Qy   2227 CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTT 2220

Qy   2287 CAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTT 2280

Qy   2347 ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG 2340

Qy   2407 AGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCT 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCT 2400

Qy   2467 GTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACA 2460

Qy   2527 GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAA 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAA 2520

Qy   2587 GCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC 2580

Qy   2647 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGC 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGC 2640

Qy   2707 CCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGAT 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGAT 2700

Qy   2767 CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAG 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAG 2760

Qy   2827 CATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGT 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGT 2820

Qy   2887 CATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 2880

Qy   2947 CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 3006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 2940

Qy   3007 CACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 3000

Qy   3067 GCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 3126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 3060

Qy   3127 GGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCT 3186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCT 3120

Qy   3187 CTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3180

Qy   3247 TATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 3306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 3240

Qy   3307 CCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 3366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 3300

Qy   3367 CCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCT 3426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 CCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCT 3360

Qy   3427 CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGAT 3486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGAT 3420

Qy   3487 TCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA 3546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA 3480

Qy   3547 GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA 3606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA 3540

Qy   3607 TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC 3666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC 3600

Qy   3667 CCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 3726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 3660

Qy   3727 AAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 AAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3720

Qy   3787 CATTGTGGGGCCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CATTGTGGGGCCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3780

Qy   3847 GGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3840

Qy   3907 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT 3966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT 3900

Qy   3967 CAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGA 4026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGA 3960

Qy   4027 GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 4086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 4020

Qy   4087 GGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4080

Qy   4147 GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4140

Qy   4207 AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT 4266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT 4200

Qy   4267 TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACA 4326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    4201 TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGGTGGCCCAGGGACA 4260

Qy    4327 GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC 4386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC 4320

Qy    4387 CATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGA 4446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4321 CATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGA 4380

Qy    4447 AGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGGCCCCTTCATCGCGTCC 4506
           |||||||||||||||||||||||::: ::|:||||||||||||||||||||||||||||
Db    4381 AGTCTCTTTTCTTTAGAGCATTGCCMYKGMMTKCCTGGGGCGGGCCCCTTCATCGCGTCC 4440

Qy    4507 TCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4441 TCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4500

Qy    4567 GTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGT 4626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4501 GTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGT 4560

Qy    4627 AAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTAT 4686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4561 AAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTAT 4620

Qy    4687 AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCT 4746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4621 AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCT 4680

Qy    4747 GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4681 GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4740

Qy    4807 TGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
           |||||||||||||||||||||||||||||||||||||||||||
Db    4741 TGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4781


RESULT   4
US-08-463-092B-3
; Sequence 3, Application US/08463092B
; Patent No. 5766880
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULES ENCODING
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,092B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-0CT-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-0CT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1546
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-463-092B-3


  Query Match             10.5%;  Score 511.2;  DB 1;  Length 5011;
  Best Local Similarity   52.5%;  Pred. No. 7.6e-123;
  Matches 1367;  Conservative    0;  Mismatches 1178;  Indels   59;  Gaps    9;

Qy    1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
           ||||| ||||||||||||   | ||    |      |||||| |  |||||    |   |||
Db    2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy    1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
           |  || |||    |||| |   |    |||   |||||  | |||||  | || ||  |
Db    2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTCGTCCCTGCTC 2259

Qy    1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
           |||||| | || |   |||||       | |||||   | | || ||||  ||  || | |
Db    2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy    1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
           || |||||| | |||||||||||||| |  |||| | ||||  |||| ||||||||| |||
Db    2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy    2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
           ||     |    || ||| |   |||| || ||| | |   |||  |||    ||
Db    2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy    2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
           |||||||  || || |||||  | || | ||| |||||||| |||   || |  ||||||
Db    2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy    2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
             || || |||   ||| |  | ||||| |||||||| ||||     ||     |||
Db    2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy    2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
           ||| || | || || ||||||   ||  | |||||||||||||| || ||||||||  |
Db    2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy    2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
           | ||  ||      |  |      || |||  ||||||     | || || || |||
Db    2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy    2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
             |   ||| ||    |   || |   | ||| ||||||  |  |||   ||  | ||
Db    2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy    2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
```





RESULT 5
US-08-462-109A-3
; Sequence 3, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,109A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002CP4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-462-109A-3


  Query Match           10.5%;  Score 511.2;  DB 2;  Length 5011;
  Best Local Similarity  52.5%;  Pred. No. 7.6e-123;
  Matches 1367;  Conservative    0;  Mismatches 1178;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
          ||||| ||||||||||||   | ||   |     |||||| |  |||||    |    |||
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
          |  || |||    |||| |   |    |||   |||||  | |||||  | || ||  |
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTCGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
          ||||||  | || |   |||||        | |||||   | | || ||||  ||  || |
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
          || ||||||  | ||||||||||||||  |  |||| | ||||  |||| |||||||| |||
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
          ||      |    || ||| |   |||| || ||| |  |   |||  |||    ||
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
          |||||||  || || |||||  | || | ||| |||||||| |||   || |  ||||||
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
             || || |||   ||| |  | ||||| |||||||| ||||     ||     |||
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
          ||| || | || || ||||||   ||  | ||||||||||||| || ||||||||  |
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
          | ||  ||      |  |      || |||  ||||||     | || || || |||
Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
          |   ||| ||    |   || |   | ||| ||||||  |  |||   ||  | ||
Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
          |  ||| || |  |||| ||| ||  |  | | || | ||  |||    |  |   || |
Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
                |||||      ||  | |   |||   ||        | ||    ||| |||
Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
          ||  |||| |  || |  | | ||          | ||       |||      | | | |
Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG------------------ 2615
          ||  |||| |   |  || |    |  ||  |  ||  ||
Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
          || || |  |       | |||    |||      | | || |   || |  | |||| ||
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
          | |||        |   | ||  | ||| |   |  || | | |  |    |  |
Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
            || ||   ||  || ||  |  | ||   ||  |       | | |          ||
Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
            |  || ||          ||  |     || |     ||||  |||     ||    ||
Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
          ||  |||      | | |  |   ||  |                | |||          ||
Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
          |||  |    ||          | | |  ||  ||  | |    ||||||  | | |||
Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016
          || |  || ||  | |  || ||||| ||     || ||||  || |||||   |||||||
Db   3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
          |  ||||   |  | ||| | ||||| ||  ||||   ||| |||    | | |||
Db   3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
                | ||||||||||      | |  ||   ||  |                | |||
Db   3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
                | |   ||       |    |      |  |||||||| | || |||  |   ||
Db   3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
```

```
Db    3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639

Qy    3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316

Db    3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699

Qy    3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376

Db    3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759

Qy    3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436

Db    3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819

Qy    3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496

Db    3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879

Qy    3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556

Db    3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939

Qy    3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616

Db    3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999

Qy    3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676

Db    4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGG 4056

Qy    3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736

Db    4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116

Qy    3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796

Db    4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176

Qy    3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856

Db    4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236

Qy    3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916

Db    4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296

Qy    3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976

Db    4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy    3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036

Db    4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy    4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096

Db    4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy    4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156

Db    4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy    4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216

Db    4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy    4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276

Db    4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy    4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336

Db    4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy    4337 TTTGACACCCCATCGGTCCTTCTG 4360

Db    4717 TACGGCGCCCCATCGGACCTCCTG 4740
```

RESULT 6
US-08-460-907B-3
; Sequence 3, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-0CT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-0CT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-460-907B-3

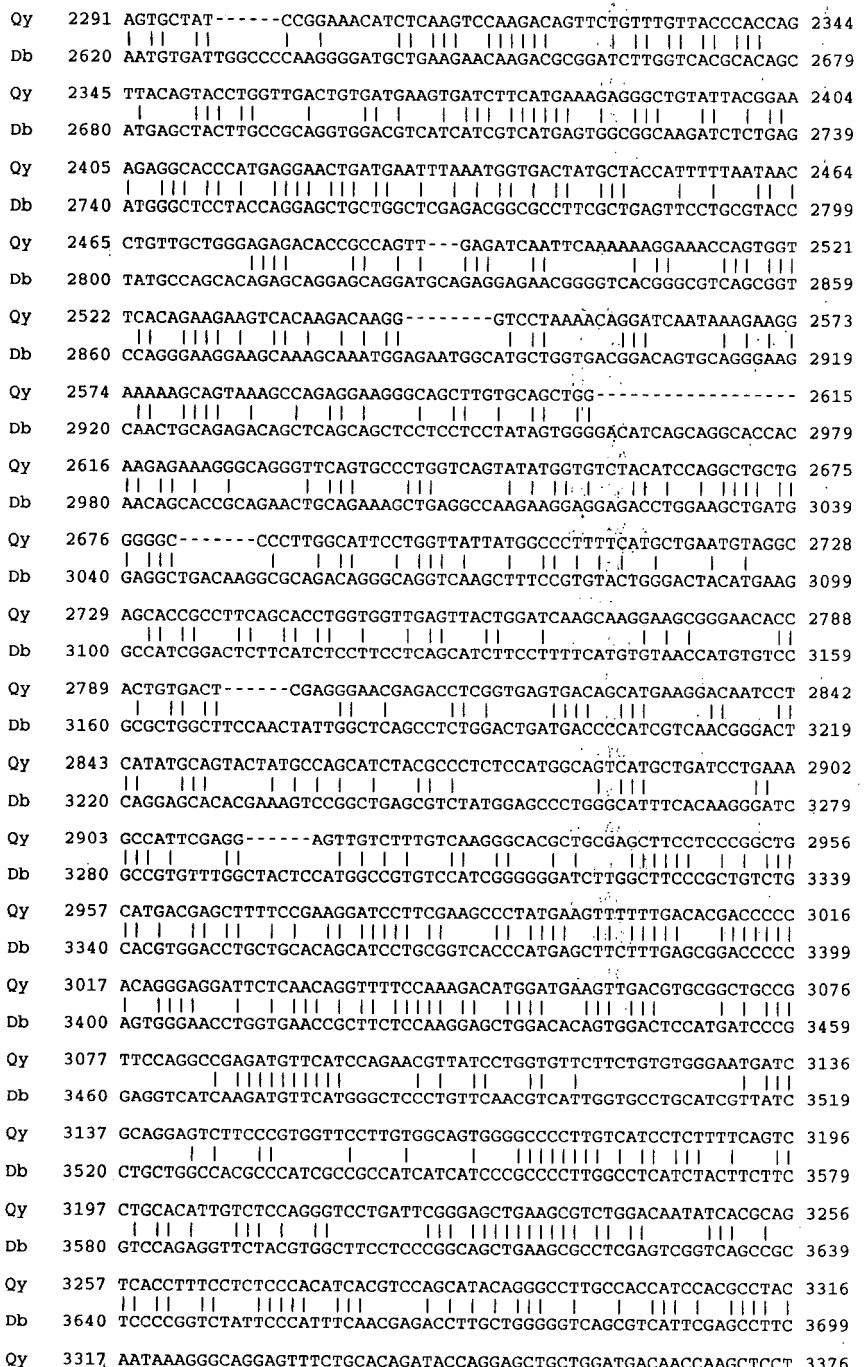
Query Match 10.5%; Score 511.2; DB 2; Length 5011;
Best Local Similarity 52.5%; Pred. No. 7.6e-123;
Matches 1367; Conservative 0; Mismatches 1178; Indels 59; Gaps 9;

```
Db   4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy   3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036

Db   4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy   4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096

Db   4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156

Db   4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216

Db   4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276

Db   4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336

Db   4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360

Db   4717 TACGGCGCCCCATCGGACCTCCTG 4740


RESULT   7
US-08-463-179A-3
; Sequence 3, Application US/08463179A
; Patent No. 6001563
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING CHEMOSENSITIZERS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,179A
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002CP8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-463-179A-3


  Query Match             10.5%;  Score 511.2;  DB 3;  Length 5011;
  Best Local Similarity   52.5%;  Pred. No. 7.6e-123;
  Matches 1367;  Conservative    0;  Mismatches 1178;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870

Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930

Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTCGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990

Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050

Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110

Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170

Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230

Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290

Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344

Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404

Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464

Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521

Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573

Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG---------------- 2615

Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
```

```
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728

Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788

Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842

Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902

Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956

Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016

Db   3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076

Db   3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136

Db   3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196

Db   3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256

Db   3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639

Qy   3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316

Db   3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699

Qy   3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376

Db   3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759

Qy   3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436

Db   3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819

Qy   3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496

Db   3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879

Qy   3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556

Db   3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939

Qy   3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616

Db   3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999

Qy   3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676

Db   4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGG 4056

Qy   3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736

Db   4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116

Qy   3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796

Db   4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176

Qy   3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856

Db   4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236

Qy   3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916

Db   4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296

Qy   3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976

Db   4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy   3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036

Db   4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy   4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096

Db   4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156

Db   4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216

Db   4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276

Db   4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336

Db   4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360

Db   4717 TACGGCGCCCCATCGGACCTCCTG 4740


RESULT   8
US-08-461-384B-3
; Sequence 3, Application US/08461384B
; Patent No. 6025473
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEINS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,384B
;      FILING DATE:  05-JUN-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
```

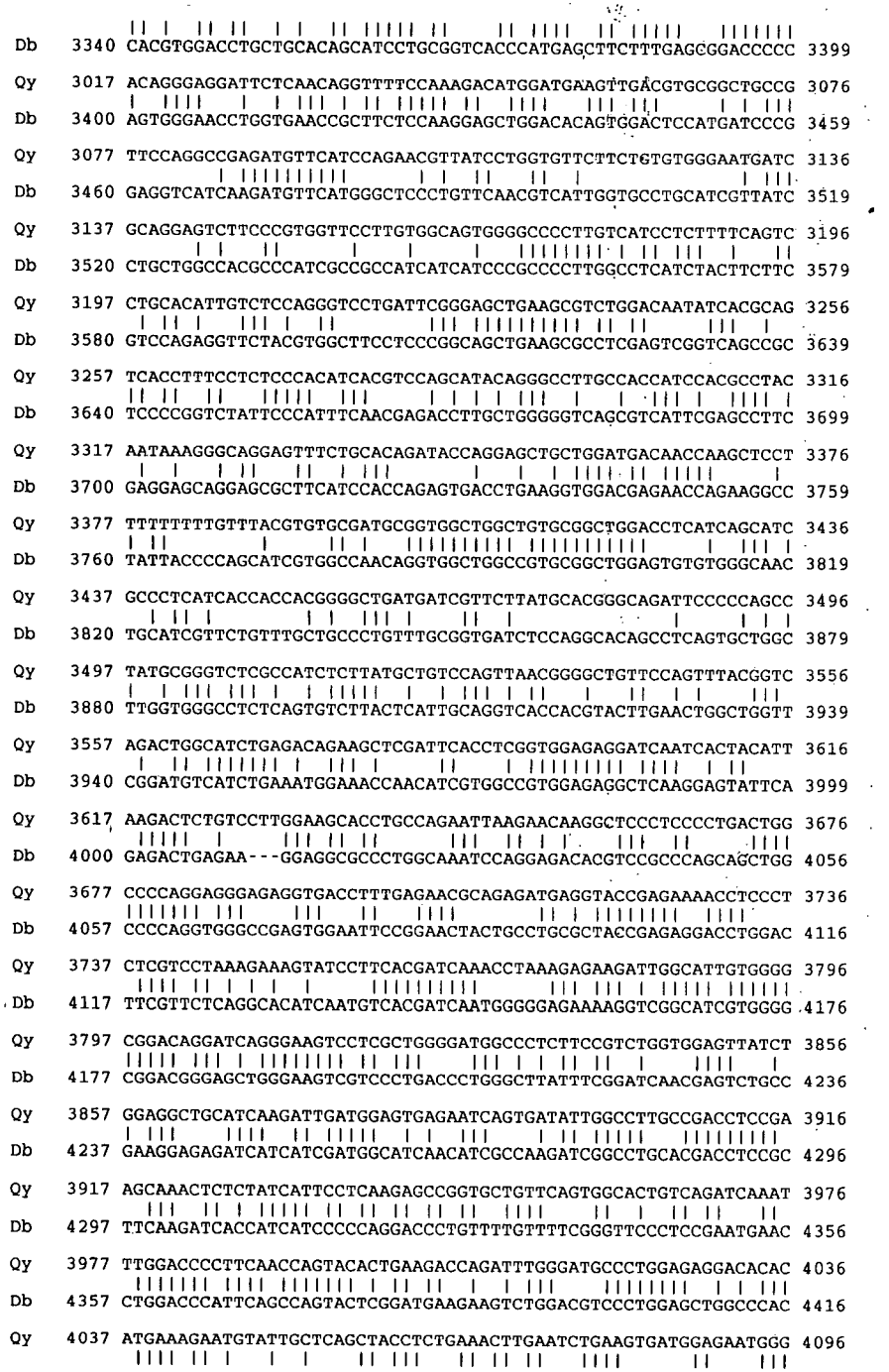
```
;       FILING DATE:  27-OCT-1992
;       APPLICATION NUMBER:  08/029,340
;       FILING DATE:  8-MAR-1993
;       APPLICATION NUMBER:  08/141,893
;       FILING DATE:  26-OCT-1993
;       APPLICATION NUMBER:  08/407,207
;       FILING DATE:  20-MAR-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Steeg, Carol Miernicki
;       REGISTRATION NUMBER:  39,539
;       REFERENCE/DOCKET NUMBER:  Q1547
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (613) 545-2342
;       TELEFAX:  (613) 545-6853
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5011 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  196..4788
US-08-461-384B-3

  Query Match             10.5%;  Score 511.2;  DB 3;  Length 5011;
  Best Local Similarity   52.5%;  Pred. No. 7.6e-123;
  Matches 1367;  Conservative    0;  Mismatches 1178;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTCGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG------------------ 2615
Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGACACGACCCCC 3016
Db   3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
Db   3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
Db   3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
Db   3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
Db   3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639

Qy   3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db   3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699

Qy   3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db   3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759

Qy   3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db   3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819

Qy   3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496
Db   3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879
```

```
Qy   3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db   3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939

Qy   3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db   3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999

Qy   3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db   4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGG 4056

Qy   3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db   4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116

Qy   3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db   4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176

Qy   3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
Db   4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236

Qy   3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916
Db   4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296

Qy   3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976
Db   4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy   3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036
Db   4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy   4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096
Db   4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
Db   4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
Db   4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
Db   4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
Db   4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360
Db   4717 TACGGCGCCCCATCGGACCTCCTG 4740


RESULT   9
US-08-141-893-1
; Sequence 1, Application US/08141893
; Patent No. 5489519
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/141,893
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923; 08/029,340
;      FILING DATE:  27-OCT-1992; 8-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5149
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-141-893-1


  Query Match             10.4%;  Score 506.4;  DB 1;  Length 5011;
  Best Local Similarity   52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619
```


Qy 2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
Db 2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679
Qy 2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
Db 2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739
Qy 2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
Db 2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799
Qy 2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
Db 2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859
Qy 2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
Db 2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919
Qy 2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG---------- 2615
Db 2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979
Qy 2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
Db 2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039
Qy 2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
Db 3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099
Qy 2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
Db 3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159
Qy 2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
Db 3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219
Qy 2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
Db 3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279
Qy 2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
Db 3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339
Qy 2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016
Db 3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399
Qy 3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
Db 3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459
Qy 3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
Db 3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519
Qy 3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
Db 3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579
Qy 3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
Db 3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639
Qy 3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db 3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699
Qy 3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db 3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759
Qy 3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db 3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819
Qy 3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496
Db 3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879
Qy 3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db 3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939
Qy 3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db 3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999
Qy 3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db 4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGG 4056
Qy 3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db 4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116
Qy 3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db 4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176
Qy 3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
Db 4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236
Qy 3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916
Db 4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296
Qy 3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976
Db 4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356
Qy 3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036
Db 4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416
Qy 4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096
Db 4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476
Qy 4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
Db 4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536
Qy 4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
Db 4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596
Qy 4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
Db 4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656
Qy 4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
Db 4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716
Qy 4337 TTTGACACCCCATCGGTCCTTCTG 4360
Db 4717 TACGGCGCCCCATCGGACCTCCTG 4740

RESULT 10

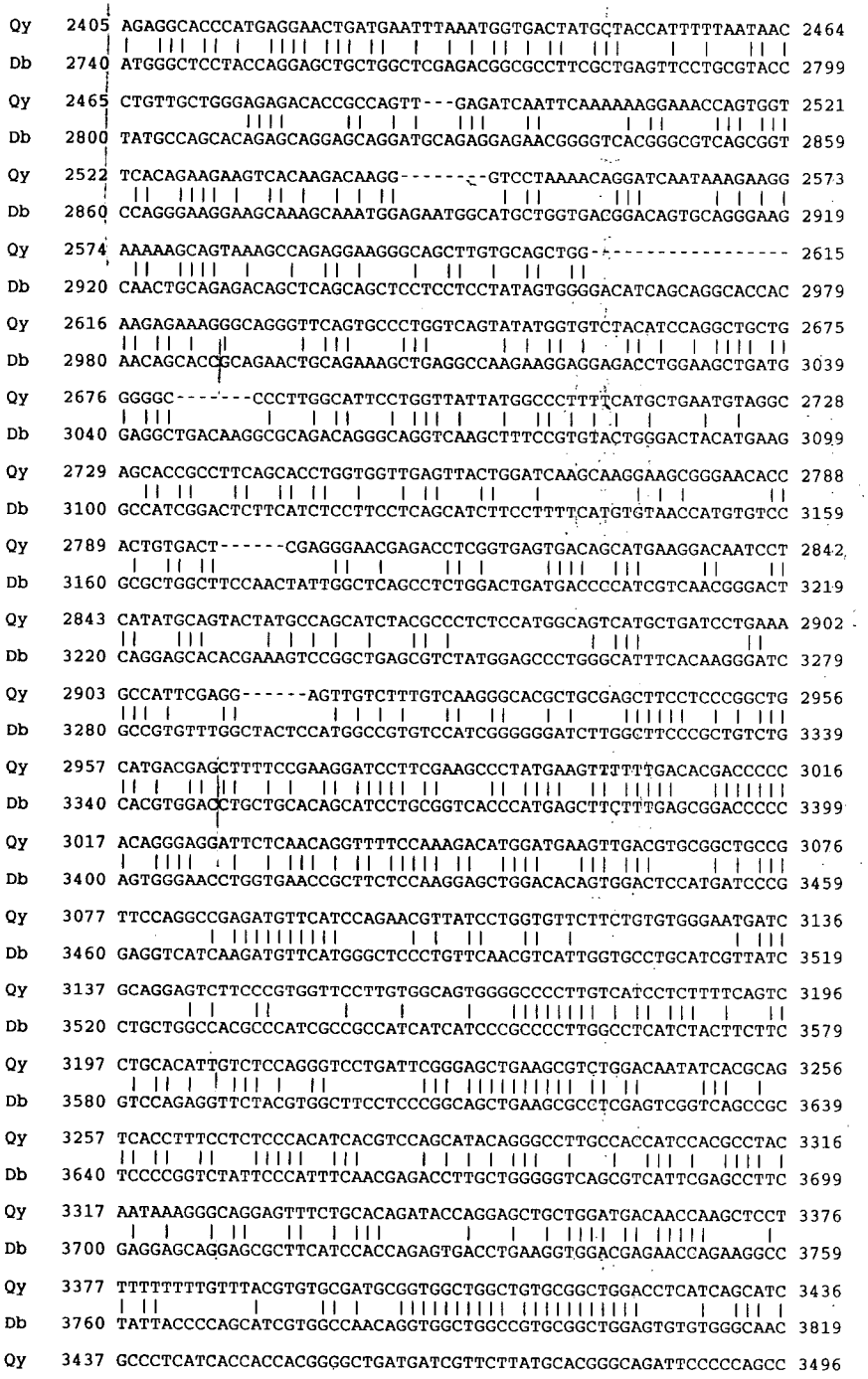
```
US-08-463-092B-1
; Sequence 1, Application US/08463092B
; Patent No. 5766880
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULES ENCODING
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,092B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1546
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-463-092B-1


  Query Match          10.4%;  Score 506.4;  DB 1;  Length 5011;
  Best Local Similarity   52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
          ||||| |||||||||||   | ||   |      |||||| |  |||||    |    |||
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
          |  || |||    |||| |   |    |||   |||||  | |||||    || ||. |
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
          |||||| | || |   |||||       | |||||   | | || |||| ||  || | |
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
          || |||||| | |||||||||||||| |  |||| | ||||  |||| |||||||| |||
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
          ||     |   || |||  |  ||||  || ||| |  |  |||   |||    ||
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
          |||||||  || || |||||  | || | ||| ||||||| |||   || |  ||||||
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
            || || |||   ||| |  | ||||| |||||||| ||||     ||     |||
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
          ||| || | || || ||||||   ||  | |||||||||||||| || ||||||||  |
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
          | ||  ||      |  |      || |||  ||||||     | || || || |||
Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
           |   ||| ||    |   || |  | ||| ||||||  |  |||   ||  | ||
Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
          |  ||| || |  |||| ||| ||  |  | | || | ||  |||    |  |   || |
Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
                  ||||     ||  | |   |||   ||      | ||   ||| |||
Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
           ||  |||| |  || |  | | ||       | ||      |||      | | | |
Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG------------------ 2615
           ||  |||| |   |  || |    |  ||  |  ||  ||
Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
          || || |  |       | |||    |||.      | | || |   || | |  |||| ||
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
          | |||         |  | ||   | ||| |   |  || | | |  |    | |
Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
            || ||   ||  || ||  |   | ||   ||   |         | | |       ||
Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
          |  || ||       ||  |    || |     |||| |||     ||   ||
Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
          ||  |||     | | | |   || |       | |||          ||
Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
          ||| |    ||        | | | |   ||  ||   | |    ||||||  | | |||
Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016
```



RESULT 11
US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

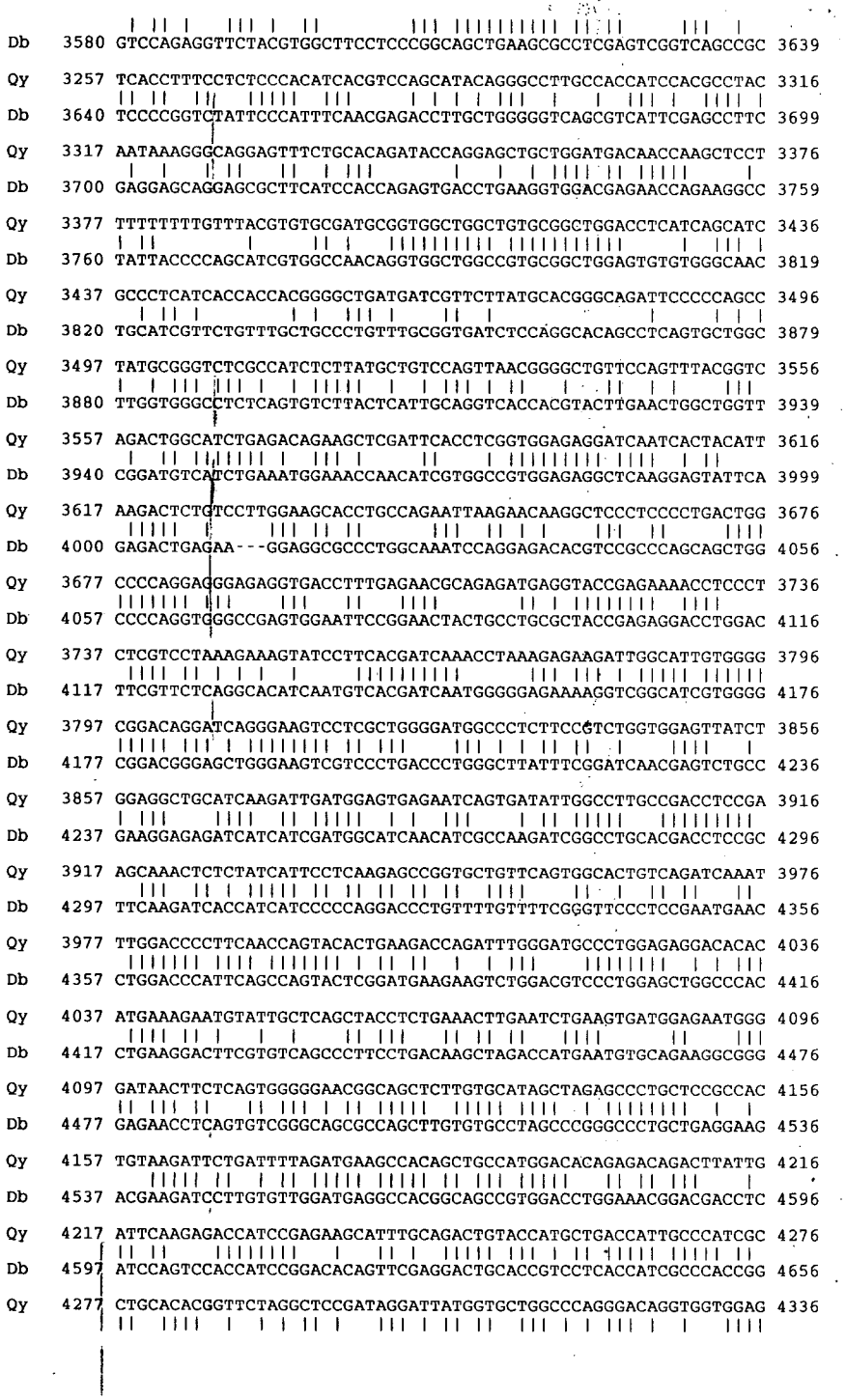
```
;       NAME/KEY:  CDS
;       LOCATION:  196..4788
US-08-462-109A-1

  Query Match             10.4%;  Score 506.4;  DB 2;  Length 5011;
  Best Local Similarity   52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTGTTACCCACCAG 2344
Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG------------------ 2615
Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTGACACGACCCCC 3016
Db   3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
Db   3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
Db   3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
Db   3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
Db   3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639

Qy   3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db   3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699

Qy   3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db   3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759

Qy   3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db   3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819

Qy   3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496
Db   3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879

Qy   3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db   3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939

Qy   3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db   3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999

Qy   3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db   4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGG 4056

Qy   3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db   4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116

Qy   3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db   4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAGGTCGGCATCGTGGGG 4176

Qy   3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
```

```
Db    4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236

Qy    3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916

Db    4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296

Qy    3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976

Db    4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy    3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036

Db    4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy    4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096

Db    4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy    4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156

Db    4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy    4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216

Db    4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy    4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276

Db    4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy    4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336

Db    4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy    4337 TTTGACACCCCATCGGTCCTTCTG 4360

Db    4717 TACGGCGCCCCATCGGACCTCCTG 4740


RESULT 12
US-08-460-907B-1
; Sequence 1, Application US/08460907B
; Patent No. 5891724
;  GENERAL INFORMATION:
;    APPLICANT:  Deeley, Roger G.
;    APPLICANT:  Cole, Susan P.C.
;    TITLE OF INVENTION:  METHODS FOR CONFERRING MULTIDRUG
;    TITLE OF INVENTION:  RESISTANCE ON A CELL
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,907B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-0CT-1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-0CT-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1551
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-460-907B-1


  Query Match           10.4%;  Score 506.4;  DB 2;  Length 5011;
  Best Local Similarity   52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy    1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870

Db    2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy    1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930

Db    2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy    1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990

Db    2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy    1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050

Db    2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy    2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110

Db    2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy    2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170

Db    2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy    2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230

Db    2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy    2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290

Db    2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy    2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344

Db    2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy    2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404

Db    2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739
```



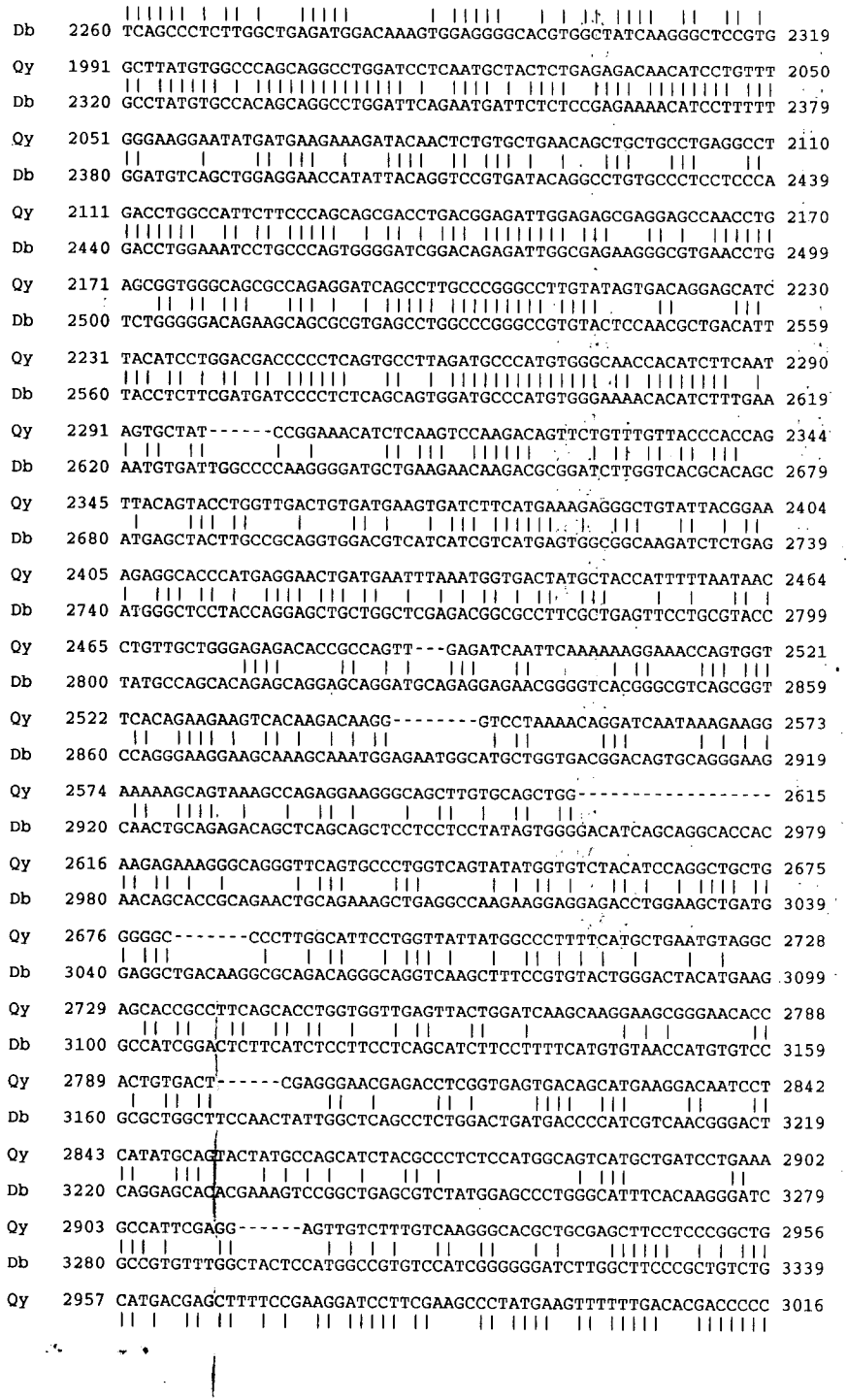
RESULT 13
US-08-463-179A-1
; Sequence 1, Application US/08463179A
; Patent No. 6001563
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
; NUMBER OF SEQUENCES: 6

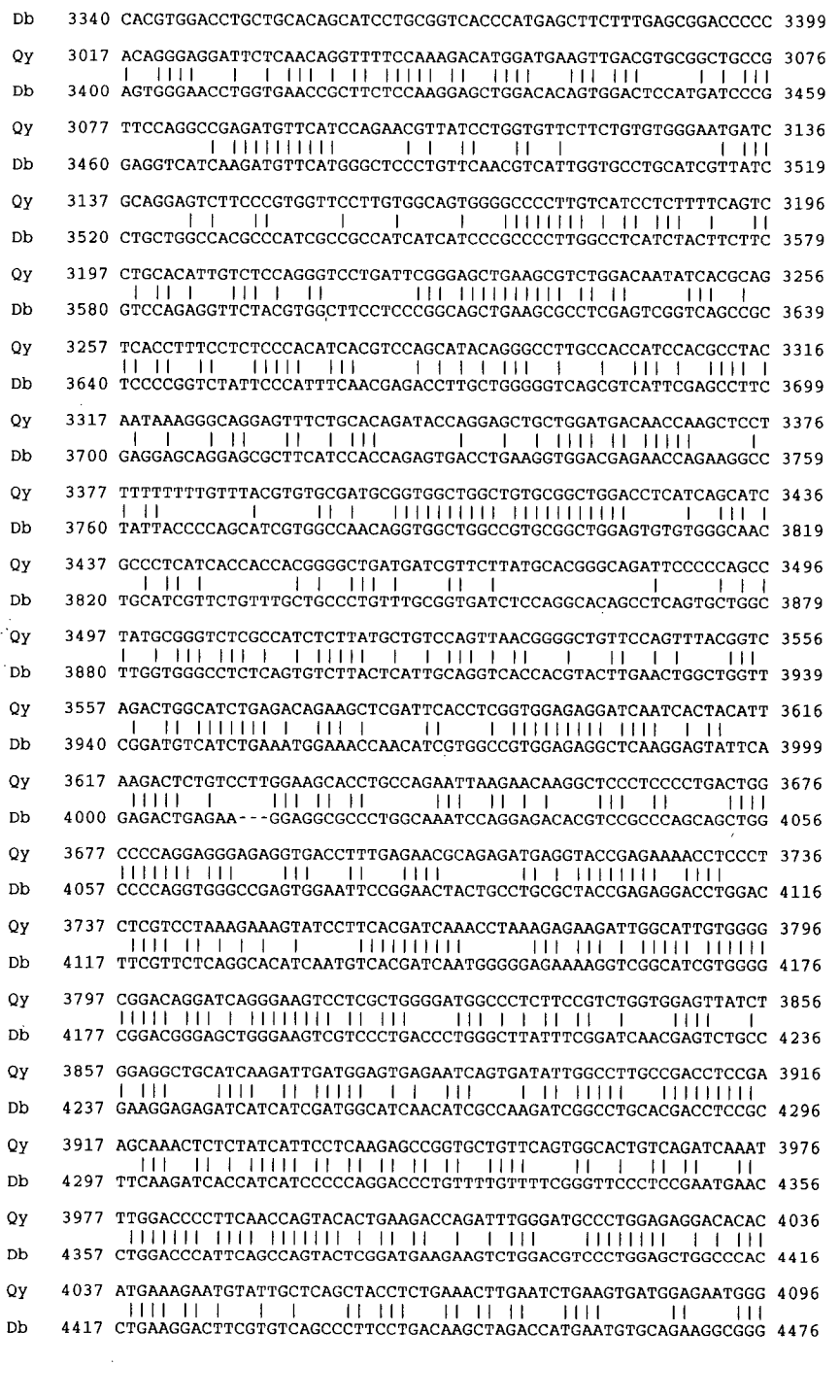
```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,179A
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002CP8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-463-179A-1

  Query Match            10.4%;  Score 506.4;  DB 3;  Length 5011;
  Best Local Similarity  52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
          ||||| ||||||||||    | ||   |      ||||||  | ||||     |    |||
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
          |  || |||    |||| |   |    |||   |||||  | |||||    || ||  |
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
          ||||||  | ||  |  |||||         | ||||||   | | || ||||  ||  || |
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
          ||  |||||| | |||||||||||||| |  |||| | ||||  |||| |||||||| |||
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
          ||      |   || |||  |  ||||  || ||| |  |   |||   |||     ||
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
          |||||||  || || |||||  | || | ||| |||||||| |||   || |  ||||||
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
             || || |||   ||| |  | ||||| |||||||| ||||     ||     |||
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
          ||| || | || || ||||||   ||  | |||||||||||||| || ||||||||  |
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
          | ||  ||      | |      || |||  ||||||     | || || || |||
Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
          |    ||| ||    |    || |   | ||| ||||||  |  |||   ||  | ||
Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
          |  ||| || |  |||| ||| ||  |  | | || | ||  |||    | |   || |
Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
                |||      || | |   |||  ||        | ||   ||| |||
Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
          ||  |||| |  || |  | | ||        | ||       |||      | | | |
Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG---------------- 2615
          ||  |||| |   |  || |   |  ||  |  ||  ||
Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
          || || |  |      | |||   |||      | | || |  || | |  | |||| ||
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
          | |||       |   | ||  | ||| |  |  || | | |  |   | |
Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
            || ||   || || ||  |  | ||  ||  |        | | |          ||
Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
          |  || ||              || |    || |    |||| |||    ||    ||
Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
          ||  |||     | | | |  || |           | |||          ||
Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
          |||  |    ||          | | | |  ||  ||  | |    ||||||  | | |||
Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016
          || |  || || |  | |  || ||||| ||     || ||||  || |||||  |||||||
Db   3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
          |  ||||   |  | ||| | || ||||| ||  ||||   ||| |||     | | |||
Db   3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
                | ||||||||||     | |  ||   ||  |                | |||
Db   3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
             | |   ||       |      |  |||||||| | || ||| |   ||
Db   3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
```



```
Db   3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639

Qy   3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db   3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699

Qy   3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db   3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759

Qy   3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db   3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819

Qy   3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496
Db   3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879

Qy   3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db   3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939

Qy   3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db   3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999

Qy   3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db   4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGG 4056

Qy   3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db   4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116

Qy   3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db   4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176

Qy   3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
Db   4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236

Qy   3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916
Db   4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296

Qy   3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976
Db   4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy   3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036
Db   4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy   4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096
Db   4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
Db   4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
Db   4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
Db   4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
```

```
Db   4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360
Db   4717 TACGGCGCCCCATCGGACCTCCTG 4740


RESULT 14
US-08-461-384B-1
; Sequence 1, Application US/08461384B
; Patent No. 6025473
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEINS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,384B
;      FILING DATE:  05-JUN-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1547
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-461-384B-1


  Query Match             10.4%;  Score 506.4;  DB 3;  Length 5011;
  Best Local Similarity   52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
```


Db 2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319
Qy 1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
Db 2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379
Qy 2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
Db 2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439
Qy 2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
Db 2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499
Qy 2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
Db 2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559
Qy 2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
Db 2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619
Qy 2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
Db 2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679
Qy 2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
Db 2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739
Qy 2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
Db 2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799
Qy 2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
Db 2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859
Qy 2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
Db 2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919
Qy 2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG---------- 2615
Db 2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979
Qy 2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
Db 2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039
Qy 2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
Db 3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099
Qy 2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
Db 3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159
Qy 2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
Db 3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219
Qy 2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
Db 3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279
Qy 2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
Db 3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339
Qy 2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016


Db 3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399
Qy 3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
Db 3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459
Qy 3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
Db 3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519
Qy 3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
Db 3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579
Qy 3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
Db 3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639
Qy 3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db 3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699
Qy 3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db 3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759
Qy 3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db 3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819
Qy 3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496
Db 3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879
Qy 3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db 3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939
Qy 3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db 3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999
Qy 3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db 4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGG 4056
Qy 3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db 4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116
Qy 3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db 4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176
Qy 3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
Db 4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236
Qy 3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916
Db 4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296
Qy 3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976
Db 4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356
Qy 3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036
Db 4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416
Qy 4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096
Db 4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

```
Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
          || ||| ||   || ||| | || |||||  ||||| ||||  | ||||||||  |  |
Db   4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
            ||||| ||  | || ||||| ||||| || ||| |||||   || || |||    |
Db   4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
          || ||   |||||||||    |   || |  ||||| ||| | || ||||| ||||| ||
Db   4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
          ||  |||| | |  | | || |   ||| | || ||  ||| | | ||| |  |   ||||
Db   4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360
          |  | | |||||||| ||| |||
Db   4717 TACGGCGCCCCATCGGACCTCCTG 4740
```

```
RESULT  15
US-08-407-207A-1
; Sequence 1, Application US/08407207A
; Patent No. 6063621
;  GENERAL INFORMATION:
;    APPLICANT:  Deeley, Roger G.
;    APPLICANT:  Cole, Susan P.C.
;    TITLE OF INVENTION:  ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/407,207A
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1512
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  196..4788
US-08-407-207A-1
```

```
  Query Match            10.4%;  Score 506.4;  DB 3;  Length 5011;
  Best Local Similarity  52.4%;  Pred. No. 1.3e-121;
  Matches 1364;  Conservative    0;  Mismatches 1181;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
          ||||| ||||||||||    | ||   |      |||||| |  |||||    |   |||
Db   2142 CACATTCACCTGGGCCA--GGAGCGACCCTCCCACACTGAATGGCATCACCTTCTCCATC 2199

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
          |  || |||    |||| |   |    |||  |||||  | |||||    || ||  |
Db   2200 CCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCCTGCTC 2259

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
          |||||| | || |   |||||       | |||||   | | || ||||  ||  || | |
Db   2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGTG 2319

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
          || |||||| | |||||||||||||| |  |||| | ||||  |||| |||||||| |||
Db   2320 GCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCTCTCCGAGAAAACATCCTTTTT 2379

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
          ||     |   || ||| |  |||| || ||| | |  |||  |||   ||
Db   2380 GGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCTGTGCCCTCCTCCCA 2439

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
          |||||||  || || |||||  | || | ||| ||||||||  |||   || |  ||||||
Db   2440 GACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCTG 2499

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
             || || |||   ||| |  | ||||| |||||||| ||||     ||     |||
Db   2500 TCTGGGGGACAGAAGCAGCGCGTGAGCCTGGCCCGGGCCGTGTACTCCAACGCTGACATT 2559

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
          ||| || | || || ||||||   ||  | |||||||||||||| || ||||||||  |
Db   2560 TACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGAA 2619

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
          | ||  ||      |  |      || ||| ||||||     | || || || |||
Db   2620 AATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGGTCACGCACAGC 2679

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
           |   ||| ||    |    || |   | ||| ||||||  |  |||   ||  | ||
Db   2680 ATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATGAGTGGCGGCAAGATCTCTGAG 2739

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
          |  ||| || |  |||| ||| ||  |  | | || | ||  |||   |  |  || |
Db   2740 ATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCCTTCGCTGAGTTCCTGCGTACC 2799

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
                |||| || | |  |||  ||       | ||  ||| |||
Db   2800 TATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAACGGGGTCACGGGCGTCAGCGGT 2859

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
           ||  |||| |  || |  | | ||         | ||      |||      | | | |
Db   2860 CCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAG 2919

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG---------------- 2615
           ||  |||| |   |  || |    |  ||  |  ||  ||
Db   2920 CAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGGACATCAGCAGGCACCAC 2979

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
          || || |  |       | |||    |||       | | || |   || |  | |||| ||
Db   2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 3039

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
          | |||        |   | ||   | ||| |   |  || | | |  |    |  |
Db   3040 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 3099

Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
            || ||   ||  || ||  |   | ||   ||  |           | | |     ||
Db   3100 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAACCATGTGTCC 3159
```

```
Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
Db   3160 GCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACT 3219

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
Db   3220 CAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATC 3279

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
Db   3280 GCCGTGTTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016
Db   3340 CACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCC 3399

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
Db   3400 AGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCG 3459

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
Db   3460 GAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATC 3519

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
Db   3520 CTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTC 3579

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
Db   3580 GTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGC 3639

Qy   3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db   3640 TCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTC 3699

Qy   3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db   3700 GAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCC 3759

Qy   3377 TTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db   3760 TATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAAC 3819

Qy   3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGCAGATTCCCCCAGCC 3496
Db   3820 TGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGC 3879

Qy   3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db   3880 TTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTT 3939

Qy   3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db   3940 CGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCA 3999

Qy   3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db   4000 GAGACTGAGAA---GGAGGCGCCCTGGCAAATCCAGGAGACACGTCCGCCCAGCAGCTGG 4056

Qy   3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db   4057 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4116

Qy   3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db   4117 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4176

Qy   3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
Db   4177 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4236

Qy   3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916

Db   4237 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4296

Qy   3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976
Db   4297 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4356

Qy   3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036
Db   4357 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4416

Qy   4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096
Db   4417 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4476

Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
Db   4477 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4536

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
Db   4537 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4596

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
Db   4597 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4656

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
Db   4657 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4716

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360
Db   4717 TACGGCGCCCCATCGGACCTCCTG 4740
```

Search completed: August 11, 2002, 09:26:39
Job time: 779 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 09:17:10 ; Search time 5627.18 Seconds
(without alignments)
18635.330 Million cell updates/sec

Title: US-09-528-031-1
Perfect score: 4847
Sequence: 1 GGCTCATGCTCGGGAGCGTG.....AAAAAAAAAAGGGCGGCCGC 4847

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US092_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US093_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US100_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US101_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4847	100.0	4847	19	US-09-528-031-1	Sequence 1, Appli
2	4800.6	99.0	5890	23	US-09-606-680-4282	Sequence 4282, Ap
3	4792.6	98.9	5838	1	PCT-US99-06644-3	Sequence 3, Appli
4	4792.6	98.9	5838	61	US-60-226-176-205	Sequence 205, App
5	4792.6	98.9	5838	62	US-60-233-468-205	Sequence 205, App
6	4792.6	98.9	5838	70	US-60-313-371-205	Sequence 205, App
7	4775.4	98.5	4781	12	US-08-843-459-1	Sequence 1, Appli
8	4304.4	88.8	4314	61	US-60-226-176-206	Sequence 206, App
9	4304.4	88.8	4314	62	US-60-233-468-206	Sequence 206, App
10	4304.4	88.8	4314	70	US-60-313-371-206	Sequence 206, App
11	3969.6	81.9	5782	71	US-60-324-185-5709	Sequence 5709, Ap
12	3748.4	77.3	5400	75	US-60-360-207-19791	Sequence 19791, A
13	3710.2	76.5	4951	66	US-60-278-258-6390	Sequence 6390, Ap
14	3707	76.5	4953	56	US-60-172-373-5777	Sequence 5777, Ap
15	2838.6	58.6	3872	30	US-09-760-470-26	Sequence 26, Appl
16	2750.6	56.7	4554	27	US-09-698-010-15045	Sequence 15045, A
17	2750.6	56.7	4554	29	US-09-726-807-3818	Sequence 3818, Ap
18	1959.8	40.4	2582	30	US-09-760-470-14	Sequence 14, Appl
19	1959.8	40.4	2582	30	US-09-760-483-180	Sequence 180, App
20	1078.6	22.3	1908	17	US-09-315-788-1747	Sequence 1747, Ap
21	1078.6	22.3	1908	17	US-09-315-788A-1747	Sequence 1747, Ap
22	1078.6	22.3	1908	30	US-09-783-514-1747	Sequence 1747, Ap
23	1078.6	22.3	1908	30	US-09-783-514A-1747	Sequence 1747, Ap
24	921	19.0	4101	30	US-09-775-685-43	Sequence 43, Appl
25	879.8	18.2	4273	37	US-10-090-280-1	Sequence 1, Appli
26	870.8	18.0	4282	37	US-10-090-280-2	Sequence 2, Appli
27	785.8	16.2	4008	30	US-09-775-685-49	Sequence 49, Appl
28	769.6	15.9	4149	28	US-09-703-253-17	Sequence 17, Appl
29	761	15.7	4074	26	US-09-668-628-2	Sequence 2, Appli
30	754.6	15.6	3660	30	US-09-775-685-45	Sequence 45, Appl
31	748.4	15.4	3753	30	US-09-775-685-47	Sequence 47, Appl

32	746.6	15.4	4162	22	US-09-557-676-930	Sequence 930, App
33	746.6	15.4	4162	37	US-10-042-938-930	Sequence 930, App
34	725.4	15.0	3189	28	US-09-703-253-5	Sequence 5, Appli
35	725.4	15.0	4083	35	US-09-934-421A-3	Sequence 3, Appli
36	725.4	15.0	4638	35	US-09-934-421A-1	Sequence 1, Appli
37	705.4	14.6	4839	71	US-60-324-185-29737	Sequence 29737, A
38	703.8	14.5	4753	17	US-09-396-885-4872	Sequence 4872, Ap
39	703.8	14.5	4753	17	US-09-396-885A-4872	Sequence 4872, Ap
40	703.8	14.5	4753	18	US-09-428-151A-9221	Sequence 9221, Ap
41	684.6	14.1	900	25	US-09-644-870-7500	Sequence 7500, Ap
42	684.6	14.1	900	25	US-09-649-162-8133	Sequence 8133, Ap
43	684.6	14.1	900	25	US-09-652-915-8826	Sequence 8826, Ap
44	659.8	13.6	3911	75	US-60-360-207-18128	Sequence 18128, A
45	651.2	13.4	4480	25	US-09-644-870-9947	Sequence 9947, Ap

ALIGNMENTS

```
RESULT   1
US-09-528-031-1
; Sequence 1, Application US/09528031
;   GENERAL INFORMATION:
;        APPLICANT: SHYJAN, Andrew
;        TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;                            POLYPEPTIDE
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD, LLP
;             STREET: 28 State Street
;             CITY: Boston
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/528,031
;             FILING DATE: 17-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Elizabeth A. Hanley
;             REGISTRATION NUMBER: 33,505
;             REFERENCE/DOCKET NUMBER: MNI-056CP
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 227-7400
;             TELEFAX: (617) 742-4214
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4847 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  116..4426
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-528-031-1


  Query Match          100.0%;  Score 4847;  DB 19;  Length 4847;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4847;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60

Qy      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120

Qy     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180

Qy     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240

Qy     241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300

Qy     301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360

Qy     361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420

Qy     421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480

Qy     481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540

Qy     541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600

Qy     601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660

Qy     661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720

Qy     721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780

Qy     781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840

Qy     841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900

Qy     901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960

Qy     961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020

Qy    1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080

Qy    1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140

Qy    1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
```

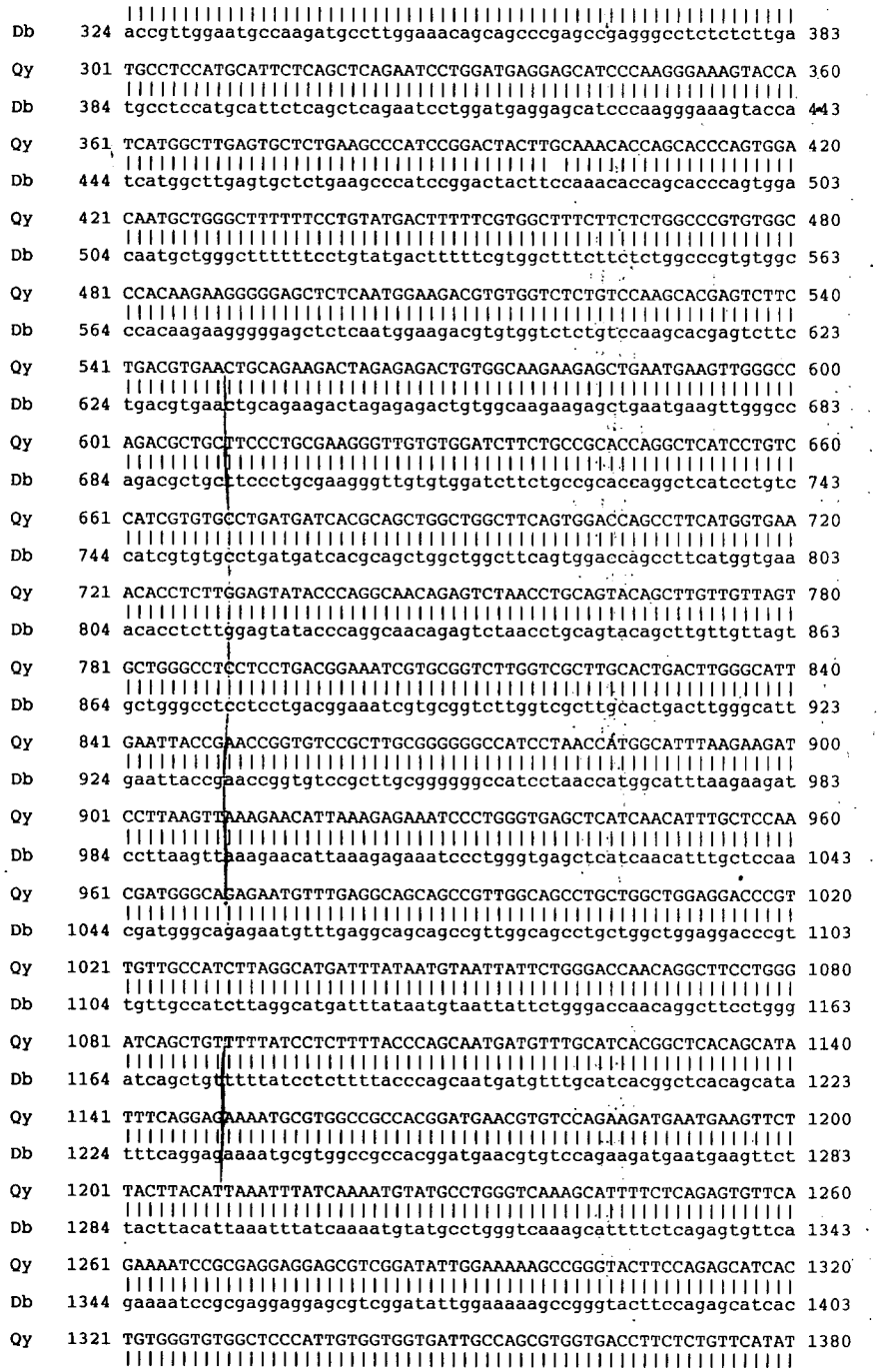
```
Qy   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260

Qy   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320

Qy   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380

Qy   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440

Qy   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500

Qy   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560

Qy   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620

Qy   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680

Qy   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740

Qy   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800

Qy   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860

Qy   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920

Qy   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980

Qy   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040

Qy   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100

Qy   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160

Qy   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220

Qy   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280

Qy   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340

Qy   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400

Qy   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460

Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520

Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580

Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640

Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700

Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760

Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820

Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880

Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940

Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000

Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060

Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120

Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
```

```
Db   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
Db   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
Db   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
Db   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
Db   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
Db   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Db   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Db   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Db   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Db   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Db   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTGTGAAACTTGAATCTGA 4080
Db   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
Db   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
Db   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
Db   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
Db   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
Db   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
Db   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
Db   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
Db   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
Db   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
Db   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
Db   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
Db   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
Qy   4801 AAGCACTGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
Db   4801 AAGCACTGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
```

RESULT 2
US-09-606-680-4282
; Sequence 4282, Application US/09606680
; GENERAL INFORMATION:
; APPLICANT: Lloyd, Clare M.
; APPLICANT: Williamson, Mark
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1131-001
; CURRENT APPLICATION NUMBER: US/09/606,680
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,227
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/141,226
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 4394
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4282
; LENGTH: 5890
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-680-4282

Query Match 99.0%; Score 4800.6; DB 23; Length 5890;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4814; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```
Qy      1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
Db     84 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 143
Qy     61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
Db    144 gaattctgatgtgaaactaacagtctgtgagccctggaacctccactcagagaagatgaa 203
Qy    121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
Db    204 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 263
Qy    181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
Db    264 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 323
Qy    241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
```


Db 324 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 383
Qy 301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
Db 384 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 443
Qy 361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
Db 444 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 503
Qy 421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
Db 504 caatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgtgtggc 563
Qy 481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
Db 564 ccacaagaaggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 623
Qy 541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
Db 624 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 683
Qy 601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
Db 684 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 743
Qy 661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
Db 744 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 803
Qy 721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
Db 804 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 863
Qy 781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
Db 864 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 923
Qy 841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
Db 924 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 983
Qy 901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
Db 984 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 1043
Qy 961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
Db 1044 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1103
Qy 1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
Db 1104 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1163
Qy 1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
Db 1164 atcagctgttttatcctctttacccagcaatgatgtttgcatcacggctcacagcata 1223
Qy 1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
Db 1224 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1283
Qy 1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
Db 1284 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1343
Qy 1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
Db 1344 gaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagagcatcac 1403
Qy 1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
Db 1404 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1463
Qy 1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
Db 1464 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1523
Qy 1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
Db 1524 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1583
Qy 1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
Db 1584 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1643
Qy 1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
Db 1644 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1703
Qy 1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
Db 1704 ccactccagtatccagaactcgcccaagctgaccccaaaatgaaaaaagacaagagggc 1763
Qy 1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
Db 1764 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1823
Qy 1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
Db 1824 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1883
Qy 1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
Db 1884 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1943
Qy 1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
Db 1944 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 2003
Qy 1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
Db 2004 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 2063
Qy 1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
Db 2064 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2123
Qy 2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
Db 2124 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2183
Qy 2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
Db 2184 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2243
Qy 2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
Db 2244 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2303
Qy 2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
Db 2304 caggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggcaacca 2363
Qy 2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
Db 2364 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2423
Qy 2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
Db 2424 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2483
Qy 2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
Db 2484 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2543

```
Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
Db   2544 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2603

Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
Db   2604 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2663

Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
Db   2664 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2723

Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
Db   2724 ctggtcagtatatggtgtctacatccaggctgctgggggccccttggcattcctggttat 2783

Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
Db   2784 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2843

Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
Db   2844 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2903

Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
Db   2904 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2963

Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
Db   2964 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 3023

Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
Db   3024 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3083

Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
Db   3084 ttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3143

Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
Db   3144 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3203

Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
Db   3204 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3263

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
Db   3264 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3323

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
Db   3324 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3383

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
Db   3384 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3443

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
Db   3444 tgacaaccaagctccttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3503

Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
Db   3504 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3563

Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
Db   3564 gcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3623

Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
Db   3624 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3683

Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
Db   3684 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3743

Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
Db   3744 tccctccccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3803

Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Db   3804 ccgagaaaacctccctctcgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3863

Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Db   3864 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3923

Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Db   3924 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3983

Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Db   3984 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 4043

Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Db   4044 cactgtcagatcaaatttggacccttcaaccagtacactgaagaccagatttgggatgc 4103

Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
Db   4104 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4163

Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
Db   4164 agtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcatagctag 4223

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
Db   4224 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4283

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
Db   4284 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4343

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
Db   4344 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4403

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
Db   4404 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4463

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
Db   4464 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4523

Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
Db   4524 tgacgaagtctcttttcttagagcattgccattccctgcctggggcgggcccc-tcatc 4582

Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
Db   4583 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4642

Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
Db   4643 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4702

Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
```

```
Db   4703 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4762

Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
Db   4763 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4822

Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
Db   4823 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttatttttatattaaaat 4882

Qy   4801 AAGCACTGTGCTAAAAAAA 4819
Db   4883 aagcactgtgctaataaca 4901
```

RESULT 3
PCT-US99-06644-3
; Sequence 3, Application PC/TUS9906644
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: PCT/US99/06644
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/079,759
; EARLIER FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/095,153
; EARLIER FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5838
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-06644-3

Query Match 98.9%; Score 4792.6; DB 1; Length 5838;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

```
Qy      1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
Db     11 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 70

Qy     61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
Db     71 gaattctgatgtgaaactaacagtctgtgagccctggaacctccgctcagagaagatgaa 130

Qy    121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
Db    131 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 190

Qy    181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
Db    191 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 250

Qy    241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
Db    251 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 310

Qy    301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
Db    311 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 370

Qy    361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
```

```
Db    371 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 430

Qy    421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
Db    431 caatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgtgtggc 490

Qy    481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
Db    491 ccacaagaaggggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 550

Qy    541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
Db    551 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 610

Qy    601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
Db    611 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 670

Qy    661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
Db    671 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 730

Qy    721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
Db    731 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 790

Qy    781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
Db    791 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 850

Qy    841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
Db    851 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 910

Qy    901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
Db    911 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 970

Qy    961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
Db    971 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1030

Qy   1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
Db   1031 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1090

Qy   1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
Db   1091 atcagctgtttttatcctctttacccagcaatgatgtttgcatcacggctcacagcata 1150

Qy   1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
Db   1151 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1210

Qy   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
Db   1211 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1270

Qy   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
Db   1271 aaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggtatcac 1330

Qy   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
Db   1331 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1390

Qy   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
Db   1391 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1450

Qy   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
Db   1451 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1510
```

```
Qy   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1511 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1570

Qy   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1571 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1630

Qy   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1631 ccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggc 1690

Qy   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1691 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1750

Qy   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1751 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1810

Qy   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1811 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1870

Qy   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1871 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1930

Qy   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1931 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 1990

Qy   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1991 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2050

Qy   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2051 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2110

Qy   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2111 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2170

Qy   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2171 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2230

Qy   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2231 caggagcatctacatcctggacgacccccagtgccttagatgcccatgtgggcaacca 2290

Qy   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2350

Qy   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2351 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2410

Qy   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2411 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2470

Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2471 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2530

Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2531 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2590

Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2591 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2650

Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2651 ctggtcagtatatggtgtctacatccaggctgctgggggcccctggcattcctggttat 2710

Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2711 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2770

Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2771 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2830

Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2831 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2890

Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 2950

Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3010

Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3011 ttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3070

Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3071 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3130

Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3131 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3190

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3191 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3250

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3251 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3310

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3311 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3370

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3371 tgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3430

Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3431 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3490

Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3491 gcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3550

Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3551 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3610

Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3611 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3670

Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
```

```
Db   3671 tccctcccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3730

Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Db   3731 ccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3790

Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Db   3791 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3850

Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Db   3851 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3910

Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Db   3911 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 3970

Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Db   3971 cactgtcagatcaaatttggacccctcaaccagtacactgaagaccagatttgggatgc 4030

Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
Db   4031 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4090

Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
Db   4091 agtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcatagctag 4150

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
Db   4151 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4210

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
Db   4211 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4270

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
Db   4271 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4330

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
Db   4331 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4390

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
Db   4391 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4450

Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
Db   4451 tgacgaagtctcttttcttagagcattgccattccctgcctggggcgggcccc-tcatc 4509

Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
Db   4510 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4569

Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
Db   4570 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4629

Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
Db   4630 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4689

Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
Db   4690 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4749

Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800

Db   4750 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttattttatattaaaat 4809

Qy   4801 AAGCACTGTGCTAAAAAAA 4819
Db   4810 aagcactgtgctaataaca 4828


RESULT   4
US-60-226-176-205
; Sequence 205, Application US/60226176
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-1 P
;  CURRENT APPLICATION NUMBER: US/60/226,176
;  CURRENT FILING DATE:  2000-08-16
;  NUMBER OF SEQ ID NOS:      2447
;  SOFTWARE:       PERL Program
; SEQ ID NO 205
;   LENGTH: 5838
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AF104942
US-60-226-176-205


  Query Match             98.9%;  Score 4792.6;  DB 61;  Length 5838;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4809;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
Db      11 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 70

Qy      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
Db      71 gaattctgatgtgaaactaacagtctgtgagccctggaacctccgctcagagaagatgaa 130

Qy     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
Db     131 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 190

Qy     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
Db     191 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 250

Qy     241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
Db     251 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 310

Qy     301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
Db     311 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 370

Qy     361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
Db     371 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 430

Qy     421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
Db     431 caatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgtgtggc 490

Qy     481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
Db     491 ccacaagaaggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 550

Qy     541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
```

```
Db    551 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 610
Qy    601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
Db    611 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 670
Qy    661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
Db    671 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 730
Qy    721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
Db    731 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 790
Qy    781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
Db    791 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 850
Qy    841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
Db    851 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 910
Qy    901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
Db    911 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 970
Qy    961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
Db    971 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1030
Qy   1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
Db   1031 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1090
Qy   1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
Db   1091 atcagctgtttttatcctctttttacccagcaatgatgtttgcatcacggctcacagcata 1150
Qy   1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
Db   1151 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1210
Qy   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
Db   1211 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1270
Qy   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
Db   1271 aaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggtatcac 1330
Qy   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
Db   1331 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1390
Qy   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
Db   1391 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1450
Qy   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
Db   1451 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1510
Qy   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
Db   1511 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1570
Qy   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
Db   1571 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1630
Qy   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
Db   1631 ccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggc 1690

Qy   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
Db   1691 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1750
Qy   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
Db   1751 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1810
Qy   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
Db   1811 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1870
Qy   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
Db   1871 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1930
Qy   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
Db   1931 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 1990
Qy   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
Db   1991 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2050
Qy   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
Db   2051 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2110
Qy   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
Db   2111 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2170
Qy   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
Db   2171 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2230
Qy   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
Db   2231 caggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggcaacca 2290
Qy   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
Db   2291 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2350
Qy   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
Db   2351 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2410
Qy   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
Db   2411 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2470
Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
Db   2471 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2530
Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
Db   2531 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2590
Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
Db   2591 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2650
Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
Db   2651 ctggtcagtatatggtgtctacatccaggctgctgggggcccccttggcattcctggttat 2710
Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
Db   2711 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2770
```

```
Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2771 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2830

Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2831 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2890

Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 2950

Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3010

Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3011 ttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3070

Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3071 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3130

Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3131 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3190

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3191 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3250

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3251 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3310

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3311 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3370

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3371 tgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3430

Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3431 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3490

Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3491 gcagattccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3550

Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3551 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3610

Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3611 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3670

Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3671 tccctcccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3730

Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   3731 ccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3790

Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3791 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3850

Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3851 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3910

Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3911 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 3970

Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3971 cactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgggatgc 4030

Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4031 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4090

Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4091 agtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcatagctag 4150

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4151 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4210

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4211 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4270

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4271 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4330

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4331 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4390

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4391 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4450

Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   4451 tgacgaagtctcttttcttagagcattgccattccctgcctggggcgggcccc-tcatc 4509

Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4510 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4569

Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4570 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4629

Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4630 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4689

Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4690 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4749

Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4750 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttattttatattaaaat 4809

Qy   4801 AAGCACTGTGCTAAAAAAA 4819
          ||||||||||||||| || |
Db   4810 aagcactgtgctaataaca 4828

RESULT   5
US-60-233-468-205
; Sequence 205, Application US/60233468
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
```

```
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Valdes, Ana
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-2 P
;  CURRENT APPLICATION NUMBER: US/60/233,468
;  CURRENT FILING DATE:  2000-09-18
;  NUMBER OF SEQ ID NOS:      2488
;  SOFTWARE:        PERL Program
; SEQ ID NO 205
;   LENGTH: 5838
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AF104942
US-60-233-468-205


  Query Match             98.9%;  Score 4792.6;  DB 62;  Length 5838;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4809;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 70

Qy      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 gaattctgatgtgaaactaacagtctgtgagccctggaacctccgctcagagaagatgaa 130

Qy     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 190

Qy     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 250

Qy     241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 310

Qy     301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 370

Qy     361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     371 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 430

Qy     421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 caatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgtgtggc 490

Qy     481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 ccacaagaaggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 550

Qy     541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     551 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 610

Qy     601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     611 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 670

Qy     661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     671 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 730

Qy     721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     731 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 790

Qy     781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     791 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 850

Qy     841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     851 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 910

Qy     901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     911 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 970

Qy     961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     971 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1030

Qy    1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1031 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1090

Qy    1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1091 atcagctgtttttatcctcttttacccagcaatgatgtttgcatcacggctcacagcata 1150

Qy    1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1151 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1210

Qy    1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1211 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1270

Qy    1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db    1271 aaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggtatcac 1330

Qy    1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1331 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1390

Qy    1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1391 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1450

Qy    1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1451 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1510

Qy    1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1511 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1570

Qy    1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1571 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1630

Qy    1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1631 ccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggc 1690

Qy    1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1691 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1750

Qy    1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1751 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1810

Qy    1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  1811 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1870
Qy  1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1871 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1930
Qy  1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1931 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 1990
Qy  1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1991 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2050
Qy  2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2051 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2110
Qy  2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2111 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2170
Qy  2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2171 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2230
Qy  2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2231 caggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggcaacca 2290
Qy  2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2291 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2350
Qy  2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2351 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2410
Qy  2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2411 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2470
Qy  2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2471 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2530
Qy  2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2531 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2590
Qy  2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2591 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2650
Qy  2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2651 ctggtcagtatatggtgtctacatccaggctgctgggggccccttggcattcctggttat 2710
Qy  2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2711 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2770
Qy  2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2771 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2830
Qy  2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2831 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2890
Qy  2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2891 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 2950

Qy  2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2951 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3010
Qy  3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3011 ttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3070
Qy  3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3071 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3130
Qy  3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3131 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3190
Qy  3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3191 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3250
Qy  3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3251 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3310
Qy  3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3311 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3370
Qy  3361 TGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3371 tgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3430
Qy  3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3431 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3490
Qy  3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3491 gcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3550
Qy  3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3551 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3610
Qy  3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3611 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3670
Qy  3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3671 tccctccccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3730
Qy  3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  3731 ccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3790
Qy  3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3791 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3850
Qy  3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3851 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3910
Qy  3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3911 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 3970
Qy  3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3971 cactgtcagatcaaatttggaccccttcaaccagtacactgaagaccagatttgggatgc 4030
```

```
Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4031 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4090

Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4091 agtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcatagctag 4150

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4151 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4210

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4211 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4270

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4271 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4330

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4331 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4390

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4391 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4450

Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4451 tgacgaagtctcttttctttagagcattgccattccctgcctggggcgggcccc-tcatc 4509

Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4510 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4569

Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4570 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4629

Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4630 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4689

Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4690 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4749

Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4750 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttattttatattaaaat 4809

Qy   4801 AAGCACTGTGCTAAAAAAA 4819
          ||||||||||||||| || |
Db   4810 aagcactgtgctaataaca 4828
```

```
RESULT   6
US-60-313-371-205
; Sequence 205, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
;  SOFTWARE: PERL Program
; SEQ ID NO 205
;   LENGTH: 5838
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AF104942
US-60-313-371-205

  Query Match             98.9%;  Score 4792.6;  DB 70;  Length 5838;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4809;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 70

Qy      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      71 gaattctgatgtgaaactaacagtctgtgagccctggaacctccgctcagagaagatgaa 130

Qy     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 190

Qy     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 250

Qy     241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 310

Qy     301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 370

Qy     361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     371 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 430

Qy     421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 caatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgtgtggc 490

Qy     481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 ccacaagaagggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 550

Qy     541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     551 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 610

Qy     601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     611 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 670

Qy     661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     671 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 730

Qy     721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     731 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 790

Qy     781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     791 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 850

Qy     841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     851 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 910

Qy     901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
```


Db 911 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 970
Qy 961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
Db 971 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1030
Qy 1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
Db 1031 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1090
Qy 1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
Db 1091 atcagctgtttttatcctcttttacccagcaatgatgtttgcatcacggctcacagcata 1150
Qy 1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
Db 1151 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1210
Qy 1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
Db 1211 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1270
Qy 1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
Db 1271 aaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggtatcac 1330
Qy 1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
Db 1331 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1390
Qy 1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
Db 1391 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1450
Qy 1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
Db 1451 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1510
Qy 1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
Db 1511 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1570
Qy 1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
Db 1571 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1630
Qy 1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
Db 1631 ccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggc 1690
Qy 1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
Db 1691 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1750
Qy 1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
Db 1751 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1810
Qy 1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
Db 1811 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1870
Qy 1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
Db 1871 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1930
Qy 1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
Db 1931 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 1990
Qy 1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
Db 1991 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2050
Qy 2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
Db 2051 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2110
Qy 2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
Db 2111 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2170
Qy 2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
Db 2171 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2230
Qy 2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
Db 2231 caggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggcaacca 2290
Qy 2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
Db 2291 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2350
Qy 2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
Db 2351 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2410
Qy 2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
Db 2411 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2470
Qy 2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
Db 2471 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2530
Qy 2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
Db 2531 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2590
Qy 2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
Db 2591 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2650
Qy 2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
Db 2651 ctggtcagtatatggtgtctacatccaggctgctgggggcccccttggcattcctggttat 2710
Qy 2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
Db 2711 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2770
Qy 2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
Db 2771 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2830
Qy 2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
Db 2831 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2890
Qy 2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
Db 2891 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 2950
Qy 2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
Db 2951 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3010
Qy 3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
Db 3011 ttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3070
Qy 3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
Db 3071 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3130

```
Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3131 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3190

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3191 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3250

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3251 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3310

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3311 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3370

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3371 tgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3430

Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3431 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3490

Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3491 gcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3550

Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3551 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3610

Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3611 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3670

Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3671 tccctccccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3730

Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3731 ccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3790

Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3791 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3850

Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3851 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3910

Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3911 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 3970

Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3971 cactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgggatgc 4030

Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4031 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4090

Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4091 agtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcatagctag 4150

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4151 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4210

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4211 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4270

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4271 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4330

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4331 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4390

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4391 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4450

Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   4451 tgacgaagtctcttttctttagagcattgccattccctgcctggggcgggcccc-tcatc 4509

Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4510 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4569

Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4570 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4629

Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4630 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4689

Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4690 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4749

Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4750 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttattttatattaaaat 4809

Qy   4801 AAGCACTGTGCTAAAAAAA 4819
          ||||||||||||||| || |
Db   4810 aagcactgtgctaataaca 4828
```

```
RESULT   7
US-08-843-459-1
; Sequence 1, Application US/08843459
;  GENERAL INFORMATION:
;    APPLICANT:  SHYJAN, Andrew
;    TITLE OF INVENTION:  NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/843,459
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FENTON, Gillian M
;      REGISTRATION NUMBER:  36,508
;      REFERENCE/DOCKET NUMBER:  MIL-001
```

```
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 248-7000
;       TELEFAX:  (617) 248-7100
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4781 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  2..4360
US-08-843-459-1


  Query Match           98.5%;  Score 4775.4;  DB 12;  Length 4781;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 4773;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      67 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT 126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATAT 60

Qy     127 CGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAAC 186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAAC 120

Qy     187 CAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTT 180

Qy     247 GGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTC 306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTC 240

Qy     307 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGG 300

Qy     367 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGACAATGC 426
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     301 CTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGCACCCAGTGGACAATGC 360

Qy     427 TGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAA 486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAA 420

Qy     487 GAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTCTGACGT 546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTCTGACGT 480

Qy     547 GAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGC 606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGC 540

Qy     607 TGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGT 666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGT 600

Qy     667 GTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCT 660

Qy     727 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGG 786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGG 720

Qy     787 CCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTA 846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTA 780

Qy     847 CCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAA 906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     781 CCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAA 840

Qy     907 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGG 966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGG 900

Qy     967 GCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGC 1026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGC 960

Qy    1027 CATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC 1086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGC 1020

Qy    1087 TGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAG 1146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAG 1080

Qy    1147 GAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTA 1206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTA 1140

Qy    1207 CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAAT 1266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAAT 1200

Qy    1267 CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1260

Qy    1327 TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT 1386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCT 1320

Qy    1387 GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC 1446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGAC 1380

Qy    1447 TTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT 1506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 TTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGT 1440

Qy    1507 TGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGC 1566
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGC 1500

Qy    1567 CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC 1626
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTC 1560

Qy    1627 CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG 1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAG 1620

Qy    1687 GGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA 1746
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGA 1680

Qy    1747 GCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG 1806
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGG 1740

Qy    1807 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGA 1800

Qy    1867 GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT 1926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCT 1860

Qy    1927 CATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC 1986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAAC 1920
```

```
Qy   1987 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 2046
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCT 1980

Qy   2047 GTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAG 2106
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAG 2040

Qy   2107 GCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAA 2166
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAA 2100

Qy   2167 CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAG 2226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAG 2160

Qy   2227 CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTT 2286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTT 2220

Qy   2287 CAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTT 2346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTT 2280

Qy   2347 ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG 2406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAG 2340

Qy   2407 AGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCT 2466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCT 2400

Qy   2467 GTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACA 2526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACA 2460

Qy   2527 GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAA 2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAA 2520

Qy   2587 GCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC 2646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTC 2580

Qy   2647 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGC 2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGC 2640

Qy   2707 CCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGAT 2766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGAT 2700

Qy   2767 CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAG 2826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAG 2760

Qy   2827 CATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGT 2886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGT 2820

Qy   2887 CATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTC 2880

Qy   2947 CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 3006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 CTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGA 2940

Qy   3007 CACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGT 3000

Qy   3067 GCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 3126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGT 3060

Qy   3127 GGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCT 3186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCT 3120

Qy   3187 CTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 CTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAA 3180

Qy   3247 TATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 3306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCAT 3240

Qy   3307 CCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 3366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAA 3300

Qy   3367 CCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCT 3426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 CCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCT 3360

Qy   3427 CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGAT 3486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGAT 3420

Qy   3487 TCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA 3546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCA 3480

Qy   3547 GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA 3606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAA 3540

Qy   3607 TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC 3666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTC 3600

Qy   3667 CCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 3726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGA 3660

Qy   3727 AAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 AAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGG 3720

Qy   3787 CATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGT 3780

Qy   3847 GGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGC 3840

Qy   3907 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT 3966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 CGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGT 3900

Qy   3967 CAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGA 4026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGA 3960

Qy   4027 GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 4086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 GAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGAT 4020

Qy   4087 GGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCT 4080

Qy   4147 GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4206
```

```
Db   4081 GCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGAC 4140

Qy   4207 AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT 4266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCAT 4200

Qy   4267 TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACA 4326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 TGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACA 4260

Qy   4327 GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC 4386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGC 4320

Qy   4387 CATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGA 4446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 CATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGA 4380

Qy   4447 AGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCC 4506
          |||||||||||||||||||||||::: ::|:||||||||||||||||||||||||||||
Db   4381 AGTCTCTTTTCTTTAGAGCATTGCCMYKGMMTKCCTGGGGCGGGCCCCTTCATCGCGTCC 4440

Qy   4507 TCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 TCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTT 4500

Qy   4567 GTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGT 4626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 GTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGT 4560

Qy   4627 AAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTAT 4686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTAT 4620

Qy   4687 AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCT 4746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 AATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCT 4680

Qy   4747 GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCAC 4740

Qy   4807 TGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4847
          |||||||||||||||||||||||||||||||||||||||||||
Db   4741 TGTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 4781


RESULT   8
US-60-226-176-206
; Sequence 206, Application US/60226176
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-1 P
;  CURRENT APPLICATION NUMBER: US/60/226,176
;  CURRENT FILING DATE:  2000-08-16
;  NUMBER OF SEQ ID NOS:      2447
;  SOFTWARE:       PERL Program
; SEQ ID NO 206
;   LENGTH: 4314
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AF104942.1
US-60-226-176-206


  Query Match             88.8%;  Score 4304.4;  DB 61;  Length 4314;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 4308;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    116 ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 atgaaggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtg 60

Qy    176 AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 agggagagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggaga 120

Qy    236 ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 actcgaccgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctct 180

Qy    296 CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cttgatgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaag 240

Qy    356 TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCA 415
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    241 taccatcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcaccca 300

Qy    416 GTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGT 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gtggacaatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgt 360

Qy    476 GTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gtggcccacaagaaggggggagctctcaatggaagacgtgtggtctctgtccaagcacgag 420

Qy    536 TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tcttctgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagtt 480

Qy    596 GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gggccagacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatc 540

Qy    656 CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ctgtccatcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatg 600

Qy    716 GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtgaaacacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttg 660

Qy    776 TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ttagtgctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgg 720

Qy    836 GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gcattgaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaag 780

Qy    896 AAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 aagatccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgc 840

Qy    956 TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA 1015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tccaacgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggagga 900

Qy   1016 CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC 1075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 cccgttgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttc 960

Qy   1076 CTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA 1135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ctgggatcagctgtttttatcctctttacccagcaatgatgtttgcatcacggctcaca 1020

Qy   1136 GCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  1021 gcatatttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaa 1080
Qy  1196 GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT 1255
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 gttcttacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagt 1140
Qy  1256 GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGC 1315
         |||||  |||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  1141 gttcaaaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggt 1200
Qy  1316 ATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT 1375
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 atcactgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgtt 1260
Qy  1376 CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTC 1435
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 catatgaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttc 1320
Qy  1436 AATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCC 1495
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 aattccatgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcc 1380
Qy  1496 TCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAG 1555
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 tcagtggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaag 1440
Qy  1556 AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC 1615
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 aacaaaccagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggac 1500
Qy  1616 TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG 1675
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 tcctcccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaag 1560
Qy  1676 AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG 1735
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 agggcttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcg 1620
Qy  1736 GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAA 1795
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 gtgctggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaa 1680
Qy  1796 GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC 1855
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 gaggaagaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagc 1740
Qy  1856 ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA 1915
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 atcgatctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtgga 1800
Qy  1916 AAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA 1975
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 aaaacctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgca 1860
Qy  1976 ATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA 2035
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 atcagtggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgaga 1920
Qy  2036 GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGC 2095
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 gacaacatcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagc 1980
Qy  2096 TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAG 2155
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 tgctgcctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagag 2040
Qy  2156 CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTAT 2215
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 cgaggagccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtat 2100
Qy  2216 AGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGC 2275
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 agtgacaggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggc 2160

Qy  2276 AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT 2335
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 aaccacatcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgtt 2220
Qy  2336 ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT 2395
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 acccaccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgt 2280
Qy  2396 ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT 2455
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 attacggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatt 2340
Qy  2456 TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC 2515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 tttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaacc 2400
Qy  2516 AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAA 2575
         |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  2401 agtggttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaa 2460
Qy  2576 AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA 2635
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 aaagcagtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttca 2520
Qy  2636 GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTG 2695
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 gtgccctggtcagtatatggtgtctacatccaggctgctgggggcccccttggcattcctg 2580
Qy  2696 GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG 2755
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 gttattatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttg 2640
Qy  2756 AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG 2815
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 agttactggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcg 2700
Qy  2816 GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC 2875
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 gtgagtgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctc 2760
Qy  2876 TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG 2935
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 tccatggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacg 2820
Qy  2936 CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG 2995
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 ctgcgagcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatg 2880
Qy  2996 AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT 3055
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 aagtttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggat 2940
Qy  3056 GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTG 3115
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 gaagttgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtg 3000
Qy  3116 TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC 3175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 ttcttctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccc 3060
Qy  3176 CTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAG 3235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 cttgtcatcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaag 3120
Qy  3236 CGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGC 3295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 cgtctggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggc 3180
Qy  3296 CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG 3355
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 cttgccaccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctg 3240
```

```
Qy   3356 CTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTG 3415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 ctggatgacaaccaagctccttttttttgtttacgtgtgcgatgcggtggctggctgtg 3300

Qy   3416 CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG 3475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 cggctggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatg 3360

Qy   3476 CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG 3535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 cacgggcagattccccagcctatgcgggtctcgccatctcttatgctgtccagttaacg 3420

Qy   3536 GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTG 3595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 gggctgttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtg 3480

Qy   3596 GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC 3655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 gagaggatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaac 3540

Qy   3656 AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG 3715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 aaggctccctccccctgactggccccaggagggagaggtgacctttgagaacgcagagatg 3600

Qy   3716 AGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA 3775
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   3601 aggtaccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaa 3660

Qy   3776 GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC 3835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 gagaagattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctc 3720

Qy   3836 TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT 3895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 ttccgtctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgat 3780

Qy   3896 ATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTC 3955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 attggccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttc 3840

Qy   3956 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 agtggcactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgg 3900

Qy   4016 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA 4075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 gatgccctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaa 3960

Qy   4076 TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA 4135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 tctgaagtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcata 4020

Qy   4136 GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG 4195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 gctagagccctgctccgccactgtaagattctgattttagatgaagccacagctgccatg 4080

Qy   4196 GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACC 4255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 gacacagagacagacttattgattcaagagaccatccgagaagcatttgcagactgtacc 4140

Qy   4256 ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG 4315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 atgctgaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctg 4200

Qy   4316 GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC 4375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 gcccagggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcc 4260

Qy   4376 CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA 4429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 cgattctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctga 4314
```

```
RESULT   9
US-60-233-468-206
; Sequence 206, Application US/60233468
; GENERAL INFORMATION:
;  APPLICANT:      Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Valdes, Ana
;  TITLE OF INVENTION:  Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE:  GX-0013-2 P
;  CURRENT APPLICATION NUMBER: US/60/233,468
;  CURRENT FILING DATE:  2000-09-18
;  NUMBER OF SEQ ID NOS:      2488
;  SOFTWARE:       PERL Program
; SEQ ID NO 206
;   LENGTH: 4314
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AF104942.1
US-60-233-468-206


  Query Match             88.8%;  Score 4304.4;  DB 62;  Length 4314;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 4308;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     116 ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 atgaaggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtg 60

Qy     176 AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA 235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 agggagagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggaga 120

Qy     236 ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT 295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 actcgaccgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctct 180

Qy     296 CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG 355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 cttgatgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaag 240

Qy     356 TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCA 415
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     241 taccatcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcaccca 300

Qy     416 GTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGT 475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 gtggacaatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgt 360

Qy     476 GTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG 535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 gtggcccacaagaaggggagctctcaatggaagacgtgtggtctctgtccaagcacgag 420

Qy     536 TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT 595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 tcttctgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagtt 480

Qy     596 GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC 655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 gggccagacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatc 540

Qy     656 CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG 715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ctgtccatcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatg 600

Qy     716 GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG 775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 gtgaaacacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttg 660
```

```
Qy    776 TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ttagtgctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgg 720

Qy    836 GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gcattgaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaag 780

Qy    896 AAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 aagatccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgc 840

Qy    956 TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA 1015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tccaacgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggagga 900

Qy   1016 CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC 1075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 cccgttgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttc 960

Qy   1076 CTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA 1135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ctgggatcagctgtttttatcctctttacccagcaatgatgtttgcatcacggctcaca 1020

Qy   1136 GCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 gcatatttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaa 1080

Qy   1196 GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT 1255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 gttcttacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagt 1140

Qy   1256 GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGC 1315
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1141 gttcaaaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggt 1200

Qy   1316 ATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT 1375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 atcactgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgtt 1260

Qy   1376 CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTC 1435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 catatgaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttc 1320

Qy   1436 AATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCC 1495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aattccatgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcc 1380

Qy   1496 TCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAG 1555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 tcagtggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaag 1440

Qy   1556 AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC 1615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 aacaaaccagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggac 1500

Qy   1616 TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG 1675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 tcctcccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaag 1560

Qy   1676 AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG 1735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 agggcttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcg 1620

Qy   1736 GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAA 1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 gtgctggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaa 1680

Qy   1796 GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC 1855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 gaggaagaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagc 1740

Qy   1856 ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA 1915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 atcgatctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtgga 1800

Qy   1916 AAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA 1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 aaaacctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgca 1860

Qy   1976 ATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA 2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 atcagtggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgaga 1920

Qy   2036 GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGC 2095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 gacaacatcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagc 1980

Qy   2096 TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAG 2155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 tgctgcctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagag 2040

Qy   2156 CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTAT 2215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 cgaggagccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtat 2100

Qy   2216 AGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGC 2275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 agtgacaggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggc 2160

Qy   2276 AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT 2335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 aaccacatcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgtt 2220

Qy   2336 ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT 2395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 acccaccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgt 2280

Qy   2396 ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT 2455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 attacggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatt 2340

Qy   2456 TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC 2515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 tttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaacc 2400

Qy   2516 AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAA 2575
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2401 agtggttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaa 2460

Qy   2576 AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA 2635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 aaagcagtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttca 2520

Qy   2636 GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTG 2695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 gtgccctggtcagtatatggtgtctacatccaggctgctgggggcccccttggcattcctg 2580

Qy   2696 GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG 2755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 gttattatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttg 2640

Qy   2756 AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG 2815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 agttactggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcg 2700

Qy   2816 GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC 2875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 gtgagtgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctc 2760

Qy   2876 TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG 2935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 tccatggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacg 2820

Qy   2936 CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG 2995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   2821 ctgcgagcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatg 2880

Qy   2996 AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT 3055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 aagtttttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggat 2940

Qy   3056 GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTG 3115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 gaagttgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtg 3000

Qy   3116 TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC 3175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ttcttctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccc 3060

Qy   3176 CTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAG 3235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 cttgtcatcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaag 3120

Qy   3236 CGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGC 3295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 cgtctggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggc 3180

Qy   3296 CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG 3355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 cttgccaccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctg 3240

Qy   3356 CTGGATGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTG 3415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 ctggatgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtg 3300

Qy   3416 CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG 3475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 cggctggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatg 3360

Qy   3476 CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG 3535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 cacgggcagattccccagcctatgcgggtctcgccatctcttatgctgtccagttaacg 3420

Qy   3536 GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTG 3595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 gggctgttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtg 3480

Qy   3596 GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC 3655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 gagaggatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaac 3540

Qy   3656 AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG 3715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 aaggctccctccctgactggccccaggagggagaggtgacctttgagaacgcagagatg 3600

Qy   3716 AGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA 3775
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   3601 aggtaccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaa 3660

Qy   3776 GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC 3835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 gagaagattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctc 3720

Qy   3836 TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT 3895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 ttccgtctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgat 3780

Qy   3896 ATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTC 3955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 attggccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttc 3840

Qy   3956 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 agtggcactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgg 3900

Qy   4016 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA 4075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 gatgccctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaa 3960

Qy   4076 TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA 4135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 tctgaagtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcata 4020

Qy   4136 GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG 4195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 gctagagccctgctccgccactgtaagattctgattttagatgaagccacagctgccatg 4080

Qy   4196 GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACC 4255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 gacacagagacagacttattgattcaagagaccatccgagaagcatttgcagactgtacc 4140

Qy   4256 ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG 4315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 atgctgaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctg 4200

Qy   4316 GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC 4375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 gcccagggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcc 4260

Qy   4376 CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA 4429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 cgattctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctga 4314


RESULT  10
US-60-313-371-206
; Sequence 206, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
;  SOFTWARE: PERL Program
; SEQ ID NO 206
;   LENGTH: 4314
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AF104942.1
US-60-313-371-206


  Query Match             88.8%;  Score 4304.4;  DB 70;  Length 4314;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 4308;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    116 ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 atgaaggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtg 60

Qy    176 AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 agggagagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggaga 120

Qy    236 ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 actcgaccgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctct 180

Qy    296 CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cttgatgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaag 240

Qy    356 TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCA 415
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    241 taccatcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcaccca 300
```

```
Qy    416 GTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGT 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gtggacaatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgt 360

Qy    476 GTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gtggcccacaagaaggggagctctcaatggaagacgtgtggtctctgtccaagcacgag 420

Qy    536 TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tcttctgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagtt 480

Qy    596 GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gggccagacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatc 540

Qy    656 CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ctgtccatcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatg 600

Qy    716 GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtgaaacacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttg 660

Qy    776 TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ttagtgctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgg 720

Qy    836 GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gcattgaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaag 780

Qy    896 AAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 aagatccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgc 840

Qy    956 TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA 1015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tccaacgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggagga 900

Qy   1016 CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC 1075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 cccgttgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttc 960

Qy   1076 CTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA 1135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ctgggatcagctgtttttatcctcttttacccagcaatgatgtttgcatcacggctcaca 1020

Qy   1136 GCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 gcatatttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaa 1080

Qy   1196 GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT 1255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 gttcttacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagt 1140

Qy   1256 GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGC 1315
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1141 gttcaaaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggt 1200

Qy   1316 ATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT 1375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 atcactgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgtt 1260

Qy   1376 CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTC 1435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 catatgaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttc 1320

Qy   1436 AATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCC 1495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aattccatgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcc 1380

Qy   1496 TCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAG 1555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 tcagtggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaag 1440

Qy   1556 AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC 1615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 aacaaaccagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggac 1500

Qy   1616 TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG 1675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 tcctcccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaag 1560

Qy   1676 AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG 1735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 agggcttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcg 1620

Qy   1736 GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAA 1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 gtgctggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaa 1680

Qy   1796 GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC 1855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 gaggaagaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagc 1740

Qy   1856 ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA 1915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 atcgatctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtgga 1800

Qy   1916 AAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA 1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 aaaacctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgca 1860

Qy   1976 ATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA 2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 atcagtggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgaga 1920

Qy   2036 GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGC 2095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 gacaacatcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagc 1980

Qy   2096 TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAG 2155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 tgctgcctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagag 2040

Qy   2156 CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTAT 2215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 cgaggagccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtat 2100

Qy   2216 AGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGC 2275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 agtgacaggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggc 2160

Qy   2276 AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT 2335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 aaccacatcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgtt 2220

Qy   2336 ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT 2395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 acccaccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgt 2280

Qy   2396 ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT 2455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 attacggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatt 2340

Qy   2456 TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC 2515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 tttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaacc 2400

Qy   2516 AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAA 2575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   2401 agtggttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaa 2460

Qy   2576 AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA 2635
```

```
Db   2461 aaagcagtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttca 2520

Qy   2636 GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTG 2695

Db   2521 gtgccctggtcagtatatggtgtctacatccaggctgctgggggcccttggcattcctg 2580

Qy   2696 GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG 2755

Db   2581 gttattatggccttttcatgctgaatgtaggcagcaccgccttcagcacctggtggttg 2640

Qy   2756 AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG 2815

Db   2641 agttactggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcg 2700

Qy   2816 GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC 2875

Db   2701 gtgagtgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctc 2760

Qy   2876 TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG 2935

Db   2761 tccatggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacg 2820

Qy   2936 CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG 2995

Db   2821 ctgcgagcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatg 2880

Qy   2996 AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT 3055

Db   2881 aagtttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggat 2940

Qy   3056 GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTG 3115

Db   2941 gaagttgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtg 3000

Qy   3116 TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC 3175

Db   3001 ttcttctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccc 3060

Qy   3176 CTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAG 3235

Db   3061 cttgtcatcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaag 3120

Qy   3236 CGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGC 3295

Db   3121 cgtctggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggc 3180

Qy   3296 CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG 3355

Db   3181 cttgccaccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctg 3240

Qy   3356 CTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTG 3415

Db   3241 ctggatgacaaccaagctccttttttttgtttacgtgtgcgatgcggtggctggctgtg 3300

Qy   3416 CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG 3475

Db   3301 cggctggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatg 3360

Qy   3476 CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG 3535

Db   3361 cacgggcagattccccagcctatgcgggtctcgccatctcttatgctgtccagttaacg 3420

Qy   3536 GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTG 3595

Db   3421 gggctgttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtg 3480

Qy   3596 GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC 3655

Db   3481 gagaggatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaac 3540

Qy   3656 AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG 3715

Db   3541 aaggctccctcccctgactggccccaggagggagaggtgacctttgagaacgcagagatg 3600

Qy   3716 AGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA 3775

Db   3601 aggtaccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaa 3660

Qy   3776 GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC 3835

Db   3661 gagaagattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctc 3720

Qy   3836 TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT 3895

Db   3721 ttccgtctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgat 3780

Qy   3896 ATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTC 3955

Db   3781 attggccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttc 3840

Qy   3956 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG 4015

Db   3841 agtggcactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgg 3900

Qy   4016 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA 4075

Db   3901 gatgccctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaa 3960

Qy   4076 TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA 4135

Db   3961 tctgaagtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcata 4020

Qy   4136 GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG 4195

Db   4021 gctagagccctgctccgccactgtaagattctgattttagatgaagccacagctgccatg 4080

Qy   4196 GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACC 4255

Db   4081 gacacagagacagacttattgattcaagagaccatccgagaagcatttgcagactgtacc 4140

Qy   4256 ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG 4315

Db   4141 atgctgaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctg 4200

Qy   4316 GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC 4375

Db   4201 gcccagggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcc 4260

Qy   4376 CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA 4429

Db   4261 cgattctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctga 4314
```

```
RESULT  11
US-60-324-185-5709
; Sequence 5709, Application US/60324185
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE: GX-0019-1 P
;  CURRENT APPLICATION NUMBER: US/60/324,185
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 35862
;  SOFTWARE: PERL Program
; SEQ ID NO 5709
;   LENGTH: 5782
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1099526.1
```

US-60-324-185-5709

Query Match 81.9%; Score 3969.6; DB 71; Length 5782;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 4108; Conservative 0; Mismatches 4; Indels 116; Gaps 2;

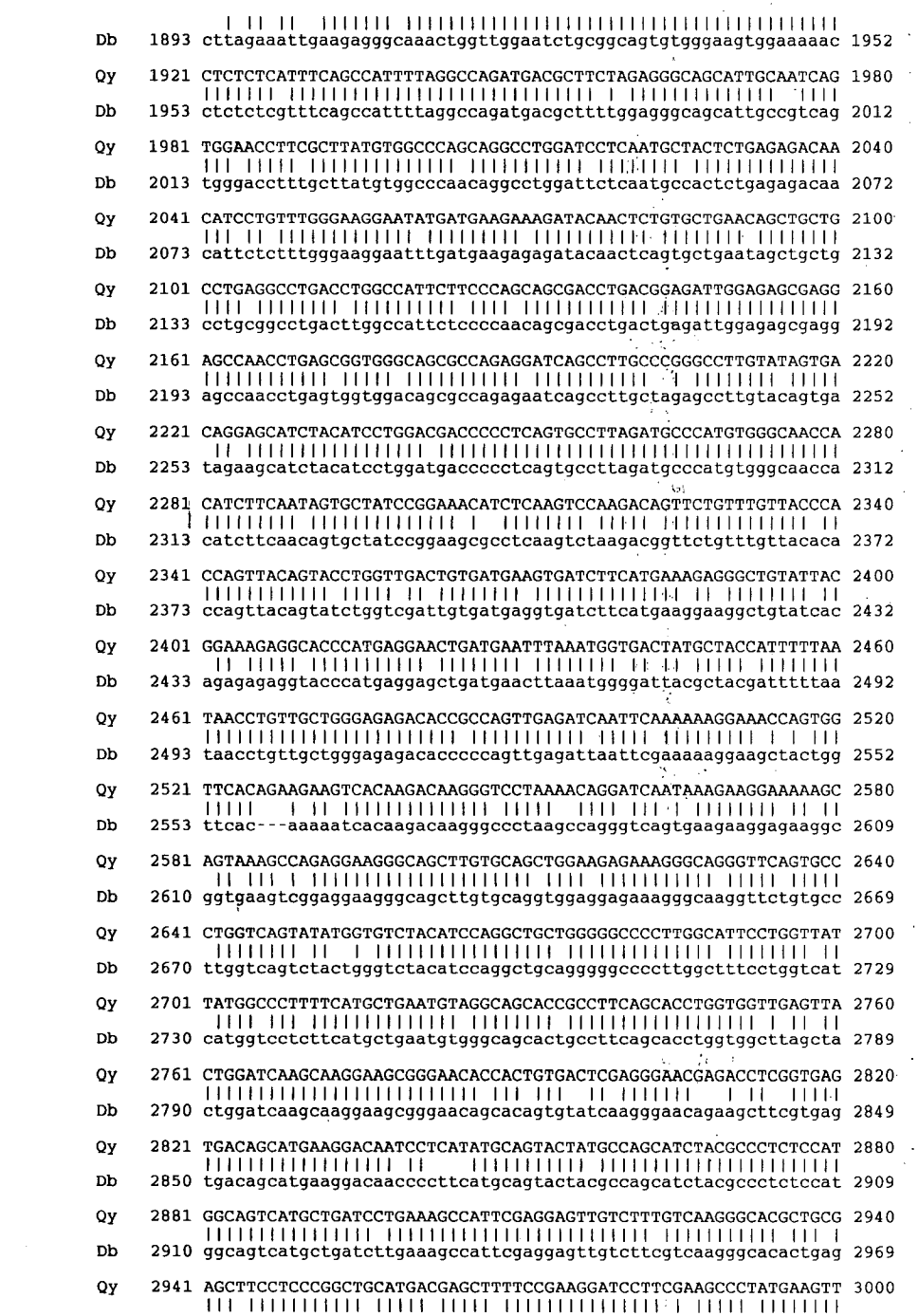
```
Qy    707 GCCTTCATGGTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTAC 766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 gccttcatggtgaaacacctcttggagtatacccaggcaacagagtctaacctgcagtac 630

Qy    767 AGCTTGTTGTTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCA 826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 agcttgttgttagtgctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgca 690

Qy    827 CTGACTTGGGCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATG 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 ctgacttgggcattgaattaccgaaccggtgtccgcttgcgggggccatcctaaccatg 750

Qy    887 GCATTTAAGAAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATC 946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 gcatttaagaagatccttaagttaaagaacattaaagagaaatccctgggtgagctcatc 810

Qy    947 AACATTTGCTCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTG 1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 aacatttgctccaacgatgggcagagaatgtttgaggcagcagccgttggcagcctgctg 870

Qy   1007 GCTGGAGGACCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCA 1066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 gctggaggacccgttgttgccatcttaggcatgatttataatgtaattattctgggacca 930

Qy   1067 ACAGGCTTCCTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCA 1126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 acaggcttcctgggatcagctgtttttatcctcttttacccagcaatgatgtttgcatca 990

Qy   1127 CGGCTCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAG 1186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 cggctcacagcatatttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaag 1050

Qy   1187 ATGAATGAAGTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTT 1246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 atgaatgaagttcttacttacattaaatttatcaaaatgtatgcctgggtcaaagcattt 1110

Qy   1247 TCTCAGAGTGTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTAC 1306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 tctcagagtgttcagaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtac 1170

Qy   1307 TTCCAGAGCATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACC 1366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 ttccagagcatcactgtgggtgtggctcccattgtggtggtgattgccagcgtggtgacc 1230

Qy   1367 TTCTCTGTTCATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTG 1426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 ttctctgttcatatgaccctgggcttcgatctgacagcagcacaggctttcacagtggtg 1290

Qy   1427 ACAGTCTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTC 1486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 acagtcttcaattccatgacttttgctttgaaagtaacaccgttttcagtaaagtccctc 1350

Qy   1487 TCAGAAGCCTCAGTGGCTGTTGACAGATTTA---------------------------- 1517
          |||||||||||||||||||||||||||||
Db   1351 tcagaagcctcagtggctgttgacagatttaagcttccttccactgtatagcctgatgtg 1410

Qy   1518 ------------------------------------------------------------ 1517

Db   1411 ttttgctacgtgagtgtacgccctaggcttgtctccctggtcttgatccagtgtctcatc 1470

Qy   1518 -------------------------AGAGTTTGTTTCTAATGGAAGAGGTTCACATGAT 1551
                                      ||||||||||||||||||||||||||||||||||||
Db   1471 tttgcacctctctcacaactcctatcagagtttgtttctaatggaagaggttcacatgat 1530

Qy   1552 AAAGAACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATG 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1531 aaagaacaaaccagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatg 1590

Qy   1612 GGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGA 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1591 ggactcctcccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaaga 1650

Qy   1672 CAAGAGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCA 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1651 caagagggcttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatca 1710

Qy   1732 GGCGGTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCC 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1711 ggcggtgctggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcc 1770

Qy   1792 CGAAGAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCA 1851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1771 cgaagaggaagaaggcaagcacatccacctgggccacctgcgcttacagaggacactgca 1830

Qy   1852 CAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAG 1911
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1831 cagcatcgatctggagatccaagagggtaaactggttggaatctgtggcagtgtgggaag 1890

Qy   1912 TGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCAT 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1891 tggaaaaacctctctcatttcagccattttaggccagatgacgcttctagagggcagcat 1950

Qy   1972 TGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCT 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1951 tgcaatcagtggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactct 2010

Qy   2032 GAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAA 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 gagagacaacatcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaa 2070

Qy   2092 CAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGG 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 cagctgctgcctgaggcctgacctggccattcttcccagcagcgacctgacggagattgg 2130

Qy   2152 AGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTT 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 agagcgaggagccaacctgagcggtgggcagcgccagaggatcagccttgcccgggcctt 2190

Qy   2212 GTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGT 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 gtatagtgacaggagcatctacatcctggacgacccccctcagtgccttagatgcccatgt 2250

Qy   2272 GGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTT 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 gggcaaccacatcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtt 2310

Qy   2332 TGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGG 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 tgttacccaccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagaggg 2370

Qy   2392 CTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTAC 2451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 ctgtattacggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctac 2430

Qy   2452 CATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGA 2511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 catttttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaaagga 2490

Qy   2512 AACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAA 2571
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   2491 aaccagtggttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaa 2550

Qy   2572 GGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGG 2631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 ggaaaaagcagtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcaggg 2610

Qy   2632 TTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATT 2691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 ttcagtgccctggtcagtatatggtgtctacatccaggctgctgggggcccccttggcatt 2670
```

```
Qy   2692 CCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTG 2751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 cctggttattatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtg 2730

Qy   2752 GTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGAC 2811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 gttgagttactggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagac 2790

Qy   2812 CTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGC 2871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 ctcggtgagtgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgc 2850

Qy   2872 CCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGG 2931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 cctctccatggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaaggg 2910

Qy   2932 CACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCC 2991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2911 cacgctgcgagcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccc 2970

Qy   2992 TATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACAT 3051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2971 tatgaagtttttgacacgacccccacagggaggattctcaacaggttttccaaagacat 3030

Qy   3052 GGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCT 3111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3031 ggatgaagttgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcct 3090

Qy   3112 GGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGG 3171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3091 ggtgttcttctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggg 3150

Qy   3172 GCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCT 3231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3151 gcccttgtcatcctcttttcagtcctgcacattgtctccagggtcctgattcgggagct 3210

Qy   3232 GAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACA 3291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3211 gaagcgtctggacaatatcacgcagtcacctttcctctcccacatcacgtccagcataca 3270

Qy   3292 GGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGA 3351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3271 gggccttgccaccatccacgcctacaataaagggcaggagtttctgcacagataccagga 3330

Qy   3352 GCTGCTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGC 3411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3331 gctgctggatgacaaccaagctccttttttttgtttacgtgtgcgatgcggtggctggc 3390

Qy   3412 TGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCT 3471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3391 tgtgcggctggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttct 3450

Qy   3472 TATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTT 3531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3451 tatgcacgggcagattccccagcctatgcgggtctcgccatctcttatgctgtccagtt 3510

Qy   3532 AACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTC 3591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3511 aacggggctgttccagtttacggtcagactggcatctgagacagaagctcgattcacctc 3570

Qy   3592 GGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAA 3651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3571 ggtggagaggatcaatcactacattaagactctgtccttggaagcacctgccagaattaa 3630

Qy   3652 GAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGA 3711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3631 gaacaaggctccctccccctgactggccccaggagggagaggtgacctttgagaacgcaga 3690

Qy   3712 GATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACC 3771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3691 gatgaggtaccgagaaaacctccctctcgtcctaaagaaagtatccttcacgatcaaacc 3750

Qy   3772 TAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGC 3831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3751 taaagagaagattggcattgtggggcggacaggatcagggaagtcctcgctggggatggc 3810

Qy   3832 CCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAG 3891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3811 cctcttccgtctggtggagttatctggaggctgcatcaagattgatggagtgagaatcag 3870

Qy   3892 TGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCT 3951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3871 tgatattggccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgct 3930

Qy   3952 GTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGAT 4011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3931 gttcagtggcactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagat 3990

Qy   4012 TTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACT 4071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3991 ttgggatgccctggagaggacacacatgaaagaatgtattgctcagctacctctgaaact 4050

Qy   4072 TGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTG 4131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4051 tgaatctgaagtgatggagaatggggataacttctcagtgggggaacggcagctcttgtg 4110

Qy   4132 CATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGC 4191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4111 catagctagagccctgctccgccactgtaagattctgattttagatgaagccacagctgc 4170

Qy   4192 CATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTG 4251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4171 catggacacagagacagacttattgattcaagagaccatccgagaagcatttgcagactg 4230

Qy   4252 TACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGT 4311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4231 taccatgctgaccattgcccatcgcctgcacacggttctaggctccgataggattatggt 4290

Qy   4312 GCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAG 4371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4291 gctggcccagggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacag 4350

Qy   4372 TTCCCGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACT 4431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4351 ttcccgattctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgact 4410

Qy   4432 CCTCCCTGTTGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGC 4491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4411 cctccctgttgacgaagtctcttttctttagagcattgccattccctgcctggggcgggc 4470

Qy   4492 CCCTTCATCGCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCA 4551
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4471 ccc-tcatcgcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagca 4529

Qy   4552 GTTCCGGATTGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTT 4611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4530 gttccggattggcttgtgtgtttcacttttagggagagtcatattttgattattgtattt 4589

Qy   4612 ATTCCATATTCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCA 4671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4590 attccatattcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttca 4649

Qy   4672 GGGAACCGTTATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATA 4731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4650 gggaaccgttattataattgtatcagaggcctataatgaagctttatacgtgtagctata 4709

Qy   4732 TCTATATATAATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTA 4791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4710 tctatatataattctgtacatagcctatatttacagtgaaaatgtaagctgtttatttta 4769

Qy   4792 TATTAAAATAAGCACTGTGCTAAAAAAA 4819
          ||||||||||||||||||||||| || |
Db   4770 tattaaaataagcactgtgctaataaca 4797
```

RESULT 12
US-60-360-207-19791
; Sequence 19791, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 19791
; LENGTH: 5400
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-19791

Query Match 77.3%; Score 3748.4; DB 75; Length 5400;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 4187; Conservative 0; Mismatches 571; Indels 16; Gaps 8;

```
Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
Db      36 gtccgatgttcgcgagcgtgcccgggctgtttgctctcgtgtggggaggctggggtgcag 95

Qy      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
Db      96 aatttctgaagtgaaaggaggagtctgca---ccctggtcctctgtgtggtgaagatgaa 152

Qy     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
Db     153 agatattgacatgggaaaagaatatatcatccccagccctgggtacagaagtgacaggga 212

Qy     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
Db     213 cagaagcgctgtaccagggcaacacagagaccccgaggaacccaggttccggagaacaag 272

Qy     241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
Db     273 atcgttggaatgccaagatgctctcgaaacagcagcccgagttgaggggctttccctgga 332

Qy     301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
Db     333 tatctctgtgcattctcatctccaaattctggacgaggagcattctaagggaaaatacca 392

Qy     361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
Db     393 ccatggtttaagtgtcctgaagcccttccggaccactaccaagcaccagcacccagtgga 452

Qy     421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
Db     453 caatgctggacttttctcctacatgacctttcatggctctctcctctggcccgagtggt 512

Qy     481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
Db     513 tcacaagaaggggagctgttaatggaggatgtgtggcctttgtccaagtatgagtcttc 572

Qy     541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
Db     573 tgatgtgaacagcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 632

Qy     601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
Db     633 agacgctgcctccctgcgaagggttgtgtggatcttttgccgcaccaggctcatcctgtc 692

Qy     661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
Db     693 catcgtgtgcctgatgatcacgcagttggctggcttcagtggaccagccttcgtggtgaa 752

Qy     721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
Db     753 gcacctcttggagtacacccaggcaacagagtctaacctgcagtacagcttgctgttagt 812

Qy     781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
Db     813 gttaggcctactcctgacagaagttgtacgctcctggtcacttgcactgacttgggcatt 872

Qy     841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
Db     873 gaattatcgaactggtgtccggttgcgggggctatcctgactatggcattcaagaagat 932

Qy     901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
Db     933 cctgaagttaaagaacattaaagaaaagtccctaggggagctcatcaatatctgctccaa 992

Qy     961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
Db     993 tgatgggcaaaggatgtttgaggcagccgctgtgggcagcttgctggctggaggacctgt 1052

Qy    1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
Db    1053 tgttgccatcttgggcatgatttataatgtaatcatcctaggacccacgggcttcctggg 1112

Qy    1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
Db    1113 atcagcggtttttatcctcttttatccagcaatgatgttcgtgtcacggctaactgcata 1172

Qy    1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
Db    1173 tttcaggagaaagtgtgtagctgccacagatgaccgtgtccagaagatgaatgaagttct 1232

Qy    1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
Db    1233 tacctacattaaattcattaaaatgtatgcctgggtcaaagcgttttctcagtgtgtgca 1292

Qy    1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
Db    1293 aaaaatccgagaggaggaacgtcggatattggagaaagccgggtactttcagagcatcac 1352

Qy    1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
Db    1353 tgttggagtggctcctattgtggtagtgatcgccagtgtggtgacgttctccgttcacat 1412

Qy    1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
Db    1413 gaccctgggcttccatctgactgcggcacaggccttcacagtggtgactgtcttcaattc 1472

Qy    1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
Db    1473 catgacttttgctttaaaagtaacaccattctcagtgaagtccctctctgaagcatcagt 1532

Qy    1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
Db    1533 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1592

Qy    1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
Db    1593 accggccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1652

Qy    1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
Db    1653 ccactccagtatacagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggc 1712

Qy    1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
Db    1713 taccaggggcaagaaagagaagtcgaggcagctgcaacacactgagcaccaggcggtgct 1772

Qy    1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
Db    1773 ggcagaacagaaaggacacctcctcctggacagtgacgagcggcccagcccggaagagga 1832

Qy    1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
Db    1833 agaaggcaagcagatccacacagggagcctgcgcctgcagaggacactgtacaacattga 1892

Qy    1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
```


Db 1893 cttagaaattgaagagggcaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1952
Qy 1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
Db 1953 ctctctcgtttcagccattttaggccagatgacgcttttggagggcagcattgccgtcag 2012
Qy 1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
Db 2013 tgggacctttgcttatgtggcccaacaggcctggattctcaatgccactctgagagacaa 2072
Qy 2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
Db 2073 cattctctttgggaaggaatttgatgaagagagatacaactcagtgctgaatagctgctg 2132
Qy 2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
Db 2133 cctgcggcctgacttggccattctccccaacagcgacctgactgagattggagagcgagg 2192
Qy 2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
Db 2193 agccaacctgagtggtggacagcgccagagaatcagccttgctagagccttgtacagtga 2252
Qy 2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
Db 2253 tagaagcatctacatcctggatgacccccctcagtgccttagatgcccatgtgggcaacca 2312
Qy 2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
Db 2313 catcttcaacagtgctatccggaagcgcctcaagtctaagacggttctgtttgttacaca 2372
Qy 2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
Db 2373 ccagttacagtatctggtcgattgtgatgaggtgatcttcatgaaggaaggctgtatcac 2432
Qy 2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
Db 2433 agagagaggtacccatgaggagctgatgaacttaaatggggattacgctacgatttttaa 2492
Qy 2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
Db 2493 taacctgttgctgggagagacacccccagttgagattaattcgaaaaaggaagctactgg 2552
Qy 2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
Db 2553 ttcac---aaaaatcacaagacaagggccctaagccagggtcagtgaagaaggagaaggc 2609
Qy 2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
Db 2610 ggtgaagtcggaggaagggcagcttgtgcaggtggaggagaaagggcaaggttctgtgcc 2669
Qy 2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
Db 2670 ttggtcagtctactgggtctacatccaggctgcagggggccccttggctttcctggtcat 2729
Qy 2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
Db 2730 catggtcctcttcatgctgaatgtgggcagcactgccttcagcacctggtggcttagcta 2789
Qy 2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
Db 2790 ctggatcaagcaaggaagcgggaacagcacagtgtatcaagggaacagaagcttcgtgag 2849
Qy 2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
Db 2850 tgacagcatgaaggacaacccctcatgcagtactacgccagcatctacgccctctccat 2909
Qy 2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
Db 2910 ggcagtcatgctgatcttgaaagccattcgaggagttgtcttcgtcaagggcacactgag 2969
Qy 2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
Db 2970 agcctcctcccggctccatgatgagctattccgaaggatccttaggagccccatgaagtt 3029
Qy 3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
Db 3030 ttttgatactaccccaacaggaaggattctcaacaggttttccaaagacatggatgaagt 3089
Qy 3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
Db 3090 ggatgtgcggctgccgttccaggctgagatgtttattcagaatgtaatcctggtgttctt 3149
Qy 3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
Db 3150 ctgtgttggaatgattgctggagtcttcccatggttcctcgtggcggtggggcctctcct 3209
Qy 3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
Db 3210 catcctcttctcacttctccacattgtctccagggtcctgattcgtgagctaaagcggtt 3269
Qy 3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
Db 3270 ggacaatatcacgcagtctcctttcctctcccacatcacgtctagcattcagggcctggc 3329
Qy 3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
Db 3330 caccatccatgcctacaacaaaaggcaggagtttttacacaggtatcaggagctcctgga 3389
Qy 3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
Db 3390 tgacaaccaggctccctttttcctgttcacctgtgcaatgaggtggctggcagtgcggct 3449
Qy 3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
Db 3450 ggacctcatcagcattgccctgattaccaccactggcctgatgattgttctcatgcatgg 3509
Qy 3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
Db 3510 acagatcccttcagcctatgcggggcttgccatctcctacgctgtgcagttaactggact 3569
Qy 3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
Db 3570 attccagttcaccgtcagactggcatcggagacagaagcacggttcacttccgtggagag 3629
Qy 3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
Db 3630 gatcaaccactatatcaagactctctctttggaagcacctgccagaatcaagaacaaggc 3689
Qy 3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
Db 3690 tcctccccatgactggccccaggagggagaagtaaccctttgagaatgcagaaatgagata 3749
Qy 3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Db 3750 ccgggaaaatctccctctggtccttaagaaagtgtccttcaccatcaagcccaaggaaaa 3809
Qy 3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Db 3810 gataggcattgtgggacgaacagggtcagggaagtcctctttggggatggccctcttccg 3869
Qy 3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Db 3870 tctggtggagctatctggaggctgcatcaagattgatggaataagaatcagtgacatcgg 3929
Qy 3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Db 3930 cctggccgacctccgaagcaaactggccatcattcctcaggagccagtgctgttcagtgg 3989
Qy 3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Db 3990 cactgtcagatcaaacctggacccttcaaccagtacacggaagaccagatctgggatgc 4049
Qy 4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
Db 4050 tctagagagaacgcacatgaaggaatgtattgcccagctacctctgaaacttgagtctga 4109

```
Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
          ||| ||||||||| ||||| |||||||| || |||||||||||||| ||||||||||| ||
Db   4110 agtaatggagaacggggacaacttctctgttggggaacggcagctgttgtgcatagcaag 4169

Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
          ||||||||| || ||||||||||||||||||||||||||||||| ||||| || ||||||||
Db   4170 agccctgctgcgtcactgtaagattctgattttagatgaagctacagccgctatggacac 4229

Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
          |||||||||||||| |||| || |||||||||||| |||||||||| ||||| ||||||||
Db   4230 agagacagacttactgatccaggagaccatccgggaagcatttgcggactgcaccatgct 4289

Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
          |||||||||||||||||||||||||| ||||| ||||| || |||||| ||||||||||||
Db   4290 gaccattgcccatcgcctgcacacagttctgggctctgacaggatcatggtgctggccca 4349

Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
          |||||||||||||||||||||||||||||||||||||||||| || |||||||| ||||
Db   4350 gggacaggtggtggagtttgacaccccatcggtccttctgtctaatgacagttcaagatt 4409

Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
          |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||| ||
Db   4410 ctatgccatgtttgctgctgcagagaacaaggtggctgtcaagggctgagtcctccc-gt 4468

Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
             |||||||||  ||| | |||||||||||||||| || |||||  |||||||    ||
Db   4469 cctcgaagtctc--ttcctcagagcattgccattctcttcctggtttgggcccc----tc 4522

Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
               |||| | ||||| | ||||||| |  |||||||| || |||| |  ||| ||||
Db   4523 atcctgtcctgctgaaacttcgcctttcccagttttatctctcacacaaccattcaggat 4582

Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
          | || ||||||||||||||||| ||| ||||||||||||||||||||||||||||| |||
Db   4583 tagc-tgtgtgtttcacttttaaggaaagtcatattttgattattgtatttattccctat 4641

Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTC-TAAAAGGTTCAGGGAACCG 4679
          |||  ||||  |||||||||||||||||||||||||||| ||| ||||||||||||||
Db   4642 tcacttaaatgaaatttagtttttgttcttaattgcactcttaagaggttcagggaacca 4701

Qy   4680 TTATTATAATTG-TATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATAT 4738
          ||| ||||| || |||||| |||||||||||||||||||| |||||||||| |||||||
Db   4702 ttactataaatgttatcagtggcctataatgaagctttatatgtgtagctatgtctatat 4761

Qy   4739 ATAATTCTGTACATAGCCTATATTTACAGTGAAA 4772
          |||||||||||||||||||||||||||||| |||
Db   4762 ataattctgtacatagcctatatttacagtaaaa 4795
```

```
RESULT  13
US-60-278-258-6390
; Sequence 6390, Application US/60278258
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION:  Polynucleotide Sequence Databases, and Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms Identified Thereby
;  FILE REFERENCE: GX-0010-1 P
;  CURRENT APPLICATION NUMBER: US/60/278,258
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 17730
;  SOFTWARE: PERL Program
; SEQ ID NO 6390
;   LENGTH: 4951
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1099526.1
US-60-278-258-6390
```

```
  Query Match             76.5%;  Score 3710.2;  DB 66;  Length 4951;
  Best Local Similarity   97.0%;  Pred. No. 0;
  Matches 3848;  Conservative    0;  Mismatches    3;  Indels  116;  Gaps    2;

Qy    968 CAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGCC 1027
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 cagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgttgttgcc 60

Qy   1028 ATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGCT 1087
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 atcttaggcatgatttataatgtaattattctgggaccaacaggcttcctgggatcagct 120

Qy   1088 GTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAGG 1147
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gtttttatcctctttacccagcaatgatgtttgcatcacggctcacagcatatttcagg 180

Qy   1148 AGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTAC 1207
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 agaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttcttacttac 240

Qy   1208 ATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAATC 1267
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 attaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttcagaaaatc 300

Qy   1268 CGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGGT 1327
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 cgcgaggaggagcgtcggatattggaaaaagccgggtacttccagagcatcactgtgggt 360

Qy   1328 GTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCTG 1387
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatatgaccctg 420

Qy   1388 GGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGACT 1447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattccatgact 480

Qy   1448 TTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGTT 1507
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 tttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagtggctgtt 540

Qy   1508 GACAGATTTA---------------------------------------------------- 1517
          ||||||||||
Db    541 gacagatttaagcttccttccactgtatagcctgatgtgttttgctacgtgagtgtacgc 600

Qy   1518 ---------------------------------------------------------------- 1517

Db    601 cctaggcttgtctccctggtcttgatccagtgtctcatctttgcacctctctcacaactc 660

Qy   1518 -----AGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGCCAGTCC 1572
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ctatcagagtttgtttctaatggaagaggttcacatgataaagaacaaaccagccagtcc 720

Qy   1573 TCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTCCAGTAT 1632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 tcacatcaagatagagatgaaaaatgccaccttggcatgggactcctcccactccagtat 780

Qy   1633 CCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAGGGGCAA 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ccagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggcttccaggggcaa 840

Qy   1693 GAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGAGCAGAA 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 gaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgctggcagagcagaa 900

Qy   1753 AGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGGCAAGCA 1812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 aggccacctcctcctggacagtgacgagcggcccagtcccgaagaggaagaaggcaagca 960

Qy   1813 CATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATCCA 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 catccacctgggccacctgcgcttacagaggacactgcacagcatcgatctggagatcca 1020
```

```
Qy   1873 AGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATTTC 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaacctctctcatttc 1080

Qy   1933 AGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTCGC 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 agccattttaggccagatgacgcttctagagggcagcattgcaatcagtggaaccttcgc 1140

Qy   1993 TTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTTGG 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ttatgtggcccagcaggcctggatcctcaatgctactctgagagacaacatcctgtttgg 1200

Qy   2053 GAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCTGA 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 gaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctgcctgaggcctga 1260

Qy   2113 CCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTGAG 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 cctggccattcttcccagcagcgacctgacggagattggagagcgaggagccaacctgag 1320

Qy   2173 CGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCTA 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 cggtgggcagcgccagaggatcagccttgcccgggccttgtatagtgacaggagcatcta 1380

Qy   2233 CATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAATAG 2292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 catcctggacgacccctcagtgccttagatgcccatgtgggcaaccacatcttcaatag 1440

Qy   2293 TGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTTACAGTA 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 tgctatccggaaacatctcaagtccaagacagttctgtttgttacccaccagttacagta 1500

Qy   2353 CCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAGAGGCAC 2412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 cctggttgactgtgatgaagtgatcttcatgaaagagggctgtattacggaaagaggcac 1560

Qy   2413 CCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCTGTTGCT 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ccatgaggaactgatgaatttaaatggtgactatgctaccatttttaataacctgttgct 1620

Qy   2473 GGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACAGAAGAA 2532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 gggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtggttcacagaagaa 1680

Qy   2533 GTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAAGCCAGA 2592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 gtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagcagtaaagccaga 1740

Qy   2593 GGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATA 2652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 ggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgccctggtcagtata 1800

Qy   2653 TGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTT 2712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 tggtgtctacatccaggctgctgggggcccttggcattcctggttattatggccctttt 1860

Qy   2713 CATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCA 2772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 catgctgaatgtaggcagcaccgccttcagcacctggtggttgagttactggatcaagca 1920

Qy   2773 AGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAGCATGAA 2832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 aggaagcgggaacaccactgtgactcgagggaacgagacctcggtgagtgacagcatgaa 1980

Qy   2833 GGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCT 2892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ggacaatcctcatatgcagtactatgccagcatctacgccctctccatggcagtcatgct 2040

Qy   2893 GATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCG 2952
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 gatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcgagcttcctcccg 2100

Qy   2953 GCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGAC 3012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 gctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtttttgacacgac 2160

Qy   3013 CCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCT 3072
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ccccacagggaggattctcaacaggttttccaaagacatggatgaagttgacgtgcggct 2220

Qy   3073 GCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAAT 3132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 gccgttccaggccgagatgttcatccagaacgttatcctggtgttcttctgtgtgggaat 2280

Qy   3133 GATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTC 3192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 gatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgtcatcctctttc 2340

Qy   3193 AGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCAC 3252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 agtcctgcacattgtctccagggtcctgattcgggagctgaagcgtctggacaatatcac 2400

Qy   3253 GCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGC 3312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 gcagtcacctttcctctcccacatcacgtccagcatacagggccttgccaccatccacgc 2460

Qy   3313 CTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGC 3372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ctacaataaagggcaggagtttctgcacagataccaggagctgctggatgacaaccaagc 2520

Qy   3373 TCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAG 3432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 tccttttttttgtttacgtgtgcgatgcggtggctggctgtgcggctggacctcatcag 2580

Qy   3433 CATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCC 3492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 catcgccctcatcaccaccacggggctgatgatcgttcttatgcacgggcagattccccc 2640

Qy   3493 AGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTAC 3552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 agcctatgcgggtctcgccatctcttatgctgtccagttaacggggctgttccagtttac 2700

Qy   3553 GGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTA 3612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ggtcagactggcatctgagacagaagctcgattcacctcggtggagaggatcaatcacta 2760

Qy   3613 CATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGA 3672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 cattaagactctgtccttggaagcacctgccagaattaagaacaaggctccctcccctga 2820

Qy   3673 CTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCT 3732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 ctggccccaggagggagaggtgacctttgagaacgcagagatgaggtaccgagaaaacct 2880

Qy   3733 CCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGT 3792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 ccctctcgtcctaaagaaagtatccttcacgatcaaacctaaagagaagattggcattgt 2940

Qy   3793 GGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTT 3852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ggggcggacaggatcagggaagtcctcgctggggatggccctcttccgtctggtggagtt 3000

Qy   3853 ATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCT 3912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 atctggaggctgcatcaagattgatggagtgagaatcagtgatattggccttgccgacct 3060

Qy   3913 CCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATC 3972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ccgaagcaaactctctatcattcctcaagagccggtgctgttcagtggcactgtcagatc 3120

Qy   3973 AAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGAC 4032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 aaatttggacccctt caaccagtacactgaagaccagatttgggatgccctggagaggac 3180

Qy   4033 ACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAA 4092
```

```
Db    3181 acacatgaaagaatgtattgctcagctacctctgaaacttgaatctgaagtgatggagaa 3240

Qy    4093 TGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCG 4152
Db    3241 tggggataacttctcagtgggggaacggcagctcttgtgcatagctagagccctgctccg 3300

Qy    4153 CCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTT 4212
Db    3301 ccactgtaagattctgattttagatgaagccacagctgccatggacacagagacagactt 3360

Qy    4213 ATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCA 4272
Db    3361 attgattcaagagaccatccgagaagcatttgcagactgtaccatgctgaccattgccca 3420

Qy    4273 TCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGT 4332
Db    3421 tcgcctgcacacggttctaggctccgataggattatggtgctggcccagggacaggtggt 3480

Qy    4333 GGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGCCATGTT 4392
Db    3481 ggagtttgacaccccatcggtccttctgtccaacgacagttcccgattctatgccatgtt 3540

Qy    4393 TGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGAAGTCTC 4452
Db    3541 tgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgttgacgaagtctc 3600

Qy    4453 TTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCCTCCTAC 4512
Db    3601 ttttctttagagcattgccattccctgcctgggcgggcccc-tcatcgcgtcctcctac 3659

Qy    4513 CGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTTGTGTGT 4572
Db    3660 cgaaaccttgcctttctcgattttatctttcgcacagcagttccggattggcttgtgtgt 3719

Qy    4573 TTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGTAAACAA 4632
Db    3720 ttcacttttagggagagtcatattttgattattgtatttattccatattcatgtaaacaa 3779

Qy    4633 AATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTATAATTGT 4692
Db    3780 aatttagtttttgttcttaattgcactctaaaaggttcagggaaccgttattataattgt 3839

Qy    4693 ATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCTGTACAT 4752
Db    3840 atcagaggcctataatgaagctttatacgtgtagctatatctatatataattctgtacat 3899

Qy    4753 AGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCACTGTGCT 4812
Db    3900 agcctatatttacagtgaaaatgtaagctgtttattttatattaaaataagcactgtgct 3959

Qy    4813 AAAAAAA 4819
Db    3960 aataaca 3966
```

```
RESULT  14
US-60-172-373-5777
; Sequence 5777, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 5777
;   LENGTH: 4953
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 221871.7
US-60-172-373-5777


  Query Match             76.5%;  Score 3707;  DB 56;  Length 4953;
  Best Local Similarity   96.9%;  Pred. No. 0;
  Matches 3846;  Conservative    0;  Mismatches    5;  Indels  116;  Gaps    2;

Qy     968 CAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGCC 1027
Db       1 cagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgttgttgcc 60

Qy    1028 ATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGCT 1087
Db      61 atcttaggcatgatttataatgtaattattctgggaccaacaggcttcctgggatcagct 120

Qy    1088 GTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAGG 1147
Db     121 gtttttatcctcttttacccagcaatgatgtttgcatcacggctcacagcatatttcagg 180

Qy    1148 AGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTAC 1207
Db     181 agaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttcttacttac 240

Qy    1208 ATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAATC 1267
Db     241 attaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttcagaaaatc 300

Qy    1268 CGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGGT 1327
Db     301 cgcgaggaggagcgtcggatattggaaaaagccgggtacttccagagcatcactgtgggt 360

Qy    1328 GTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCTG 1387
Db     361 gtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatatgaccctg 420

Qy    1388 GGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGACT 1447
Db     421 ggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattccatgact 480

Qy    1448 TTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGTT 1507
Db     481 tttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagtggctgtt 540

Qy    1508 GACAGATTTA---------------------------------------------------- 1517
Db     541 gacagatttaagcttccttccactgtatagcctgatgtgttttgctacgtgagtgtacgc 600

Qy    1518 ---------------------------------------------------------- 1517
Db     601 cctaggcttgtctccctggtcttgatccagtgtctcatctttgcacctctctcacaactc 660

Qy    1518 -----AGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGCCAGTCC 1572
Db     661 ctatcagagtttgtttctaatggaagaggttcacatgataaagaacaaaccagccagtcc 720

Qy    1573 TCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTCCAGTAT 1632
Db     721 tcacatcaagatagagatgaaaaatgccaccttggcatgggactcctcccactccagtat 780

Qy    1633 CCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAGGGGCAA 1692
Db     781 ccagaactcgcccaagctgacccccaaaatgaaaaaagacaagagggcttccaggggcaa 840

Qy    1693 GAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGAGCAGAA 1752
Db     841 gaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgctggcagagcagaa 900

Qy    1753 AGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGGCAAGCA 1812
```

```
Db    901 aggccacctcctcctggacagtgacgagcggcccagtcccgaagaggaagaaggcaagca 960

Qy   1813 CATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATCCA 1872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 catccacctgggccacctgcgcttacagaggacactgcacagcatcgatctggagatcca 1020

Qy   1873 AGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATTTC 1932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaacctctctcatttc 1080

Qy   1933 AGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTCGC 1992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 agccattttaggccagatgacgcttctagagggcagcattgcaatcagtggaaccttcgc 1140

Qy   1993 TTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTTGG 2052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ttatgtggcccagcaggcctggatcctcaatgctactctgagagacaacatcctgtttgg 1200

Qy   2053 GAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCTGA 2112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 gaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctgcctgaggcctga 1260

Qy   2113 CCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTGAG 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 cctggccattcttcccagcagcgacctgacggagattggagagcgaggagccaacctgag 1320

Qy   2173 CGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCTA 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 cggtgggcagcgccagaggatcagccttgcccgggccttgtatagtgacaggagcatcta 1380

Qy   2233 CATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAATAG 2292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 catcctggacgacccccctcagtgccttagatgcccatgtgggcaaccacatcttcaatag 1440

Qy   2293 TGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTTACAGTA 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 tgctatccggaaacatctcaagtccaagacagttctgtttgttacccaccagttacagta 1500

Qy   2353 CCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAGAGGCAC 2412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 cctggttgactgtgatgaagtgatcttcatgaaagagggctgtattacggaaagaggcac 1560

Qy   2413 CCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCTGTTGCT 2472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ccatgaggaactgatgaatttaaatggtgactatgctaccatttttaataacctgttgct 1620

Qy   2473 GGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACAGAAGAA 2532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 gggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtggttcacagaagaa 1680

Qy   2533 GTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAAGCCAGA 2592
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1681 gtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagcagtaaagccaga 1740

Qy   2593 GGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATA 2652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 ggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgccctggtcagtata 1800

Qy   2653 TGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTT 2712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 tggtgtctacatccaggctgctgggggcccccttggcattcctggttattatggccctttt 1860

Qy   2713 CATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCA 2772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 catgctgaatgtaggcagcaccgccttcagcacctggtggttgagttactggatcaagca 1920

Qy   2773 AGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAGCATGAA 2832
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 aggaagcggaaacaccactgtgactcgagggaacgagacctcggtgagtgacagcatgaa 1980

Qy   2833 GGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCT 2892
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ggacaatcctcatatgcagtactatgccagcatctacgccctctccatggcagtcatgct 2040

Qy   2893 GATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCG 2952
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 gatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcgagcttcctcccg 2100

Qy   2953 GCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGAC 3012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 gctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtttttgacacgac 2160

Qy   3013 CCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCT 3072
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ccccacagggaggattctcaacaggttttccaaagacatggatgaagttgacgtgcggct 2220

Qy   3073 GCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAAT 3132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 gccgttccaggccgagatgttcatccagaacgttatcctggtgttcttctgtgtgggaat 2280

Qy   3133 GATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTC 3192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 gatcgcaggagtcttcccgtggttccttgtggcagtggggcccttgtcatcctctttc 2340

Qy   3193 AGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCAC 3252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 agtcctgcacattgtctccagggtcctgattcgggagctgaagcgtctggacaatatcac 2400

Qy   3253 GCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGC 3312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 gcagtcacctttcctctcccacatcacgtccagcatacagggccttgccaccatccacgc 2460

Qy   3313 CTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGC 3372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ctacaataaagggcaggagtttctgcacagataccaggagctgctggatgacaaccaagc 2520

Qy   3373 TCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAG 3432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 tcctttttttttgtttacgtgtgcgatgcggtggctggctgtgcggctggacctcatcag 2580

Qy   3433 CATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCC 3492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 catcgccctcatcaccaccacggggctgatgatcgttcttatgcacgggcagattccccc 2640

Qy   3493 AGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTAC 3552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 agcctatgcgggtctcgccatctcttatgctgtccagttaacggggctgttccagtttac 2700

Qy   3553 GGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTA 3612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ggtcagactggcatctgagacagaagctcgattcacctcggtggagaggatcaatcacta 2760

Qy   3613 CATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGA 3672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 cattaagactctgtccttggaagcacctgccagaattaagaacaaggctccctccctga 2820

Qy   3673 CTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCT 3732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 ctggccccaggagggagaggtgacctttgagaacgcagagatgaggtaccgagaaaacct 2880

Qy   3733 CCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGT 3792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 ccctctcgtcctaaagaaagtatccttcacgatcaaacctaaagagaagattggcattgt 2940

Qy   3793 GGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTT 3852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 ggggcggacaggatcagggaagtcctcgctggggatggccctcttccgtctggtggagtt 3000

Qy   3853 ATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCT 3912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 atctggaggctgcatcaagattgatggagtgagaatcagtgatattggccttgccgacct 3060

Qy   3913 CCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATC 3972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ccgaagcaaactctctatcattcctcaagagccggtgctgttcagtggcactgtcagatc 3120
```

```
Qy   3973 AAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGAC 4032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 aaatttggacccccttcaaccagtacactgaagaccagatttgggatgccccggagaggac 3180

Qy   4033 ACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAA 4092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 acacatgaaagaatgtattgctcagctacctctgaaacttgaatctgaagtgatggagaa 3240

Qy   4093 TGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCG 4152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 tggggataacttctcagtgggggaacggcagctcttgtgcatagctagagccctgctccg 3300

Qy   4153 CCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTT 4212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ccactgtaagattctgattttagatgaagccacagctgccatggacacagagacagactt 3360

Qy   4213 ATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCA 4272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 attgattcaagagaccatccgagaagcatttgcagactgtaccatgctgaccattgccca 3420

Qy   4273 TCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGT 4332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 tcgcctgcacacggttctaggctccgataggattatggtgctggcccagggacaggtggt 3480

Qy   4333 GGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGCCATGTT 4392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 ggagtttgacaccccatcggtccttctgtccaacgacagttcccgattctatgccatgtt 3540

Qy   4393 TGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGAAGTCTC 4452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 tgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgttgacgaagtctc 3600

Qy   4453 TTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCCTCCTAC 4512
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   3601 ttttctttagagcattgccattccctgcctggggcgggcccc-tcatcgcgtcctcctac 3659

Qy   4513 CGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTTGTGTGT 4572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3660 cgaaaccttgcctttctcgattttatctttcgcacagcagttccggattggcttgtgtgt 3719

Qy   4573 TTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGTAAACAA 4632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3720 ttcactttagggagagtcatatttgattattgtatttattccatattcatgtaaacaa 3779

Qy   4633 AATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTATAATTGT 4692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3780 aatttagtttttgttcttaattgcactctaaaaggttcagggaaccgttattataattgt 3839

Qy   4693 ATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCTGTACAT 4752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3840 atcagaggcctataatgaagctttatacgtgtagctatatctatatataattctgtacat 3899

Qy   4753 AGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCACTGTGCT 4812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3900 agcctatatttacagtgaaaatgtaagctgtttattttatattaaaataagcactgtgct 3959

Qy   4813 AAAAAAA 4819
          || || |
Db   3960 aataaca 3966
```

RESULT 15
US-09-760-470-26
; Sequence 26, Application US/09760470
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ39
; CURRENT APPLICATION NUMBER: US/09/760,470
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26
; LENGTH: 3872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-470-26

Query Match 58.6%; Score 2838.6; DB 30; Length 3872;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2863; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

```
Qy   1951 GACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGC 2010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 gacgcttctagagggcagcattgcaatcagtggaaccttcgcttatgtggcccagcaggc 71

Qy   2011 CTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGA 2070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 ctggatcctcaatgctactctgagagacaacatcctgtttgggaaggaatatgatgaaga 131

Qy   2071 AAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAG 2130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 aagatacaactctgtgctgaacagctgctgcctgaggcctgacctggccattcttcccag 191

Qy   2131 CAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAG 2190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 cagcgacctgacggagattggagagcgaggagccaacctgagcggtgggcagcgccagag 251

Qy   2191 GATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCT 2250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 gatcagccttgcccgggccttgtatagtgacaggagcatctacatcctggacgacccccct 311

Qy   2251 CAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCT 2310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 cagtgccttagatgcccatgtgggcaaccacatcttcaatagtgctatccggaaacatct 371

Qy   2311 CAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGA 2370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 caagtccaagacagttctgtttgttacccaccagttacagtacctggttgactgtgatga 431

Qy   2371 AGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAA 2430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 agtgatcttcatgaaagagggctgtattacggaaagaggcacccatgaggaactgatgaa 491

Qy   2431 TTTAAATGGTGACTATGCTACCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGT 2490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 tttaaatggtgactatgctaccatttttaataacctgttgctgggagagacaccgccagt 551

Qy   2491 TGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCC 2550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 tgagatcaattcaaaaaaggaaaccagtggttcacagaagaagtcacaagacaagggtcc 611

Qy   2551 TAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCA 2610
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    612 taaaacaggatcagtaaagaaggaaaaagcagtaaagccagaggaagggcagcttgtgca 671

Qy   2611 GCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGC 2670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 gctggaagagaaagggcagggttcagtgccctggtcagtatatggtgtctacatccaggc 731

Qy   2671 TGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAG 2730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 tgctgggggccccttggcattcctggttattatggccctttcatgctgaatgtaggcag 791

Qy   2731 CACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCAC 2790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 caccgccttcagcacctggtggttgagttactggatcaagcaaggaagcgggaacaccac 851

Qy   2791 TGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCA 2850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 tgtgactcgagggaacgagacctcggtgagtgacagcatgaaggacaatcctcatatgca 911

Qy   2851 GTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCG 2910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    912 gtactatgccagcatctacgccctctccatggcagtcatgctgatcctgaaagccattcg 971

Qy   2911 AGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTT 2970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 aggagttgtctttgtcaagggcacgctgcgagcttcctcccggctgcatgacgagctttt 1031

Qy   2971 CCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCT 3030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 ccgaaggatccttcgaagccctatgaagtttttgacacgaccccacagggaggattct 1091

Qy   3031 CAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGAT 3090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 caacaggttttccaaagacatggatgaagttgacgtgcggctgccgttccaggccgagat 1151

Qy   3091 GTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCC 3150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 gttcatccagaacgttatcctggtgttcttctgtgtgggaatgatcgcaggagtcttccc 1211

Qy   3151 GTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTC 3210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 gtggttccttgtggcagtggggcccttgtcatcctcttttcagtcctgcacattgtctc 1271

Qy   3211 CAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTC 3270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 cagggtcctgattcgggagctgaagcgtctggacaatatcacgcagtcacctttcctctc 1331

Qy   3271 CCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGA 3330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 ccacatcacgtccagcatacagggccttgccaccatccacgcctacaataaagggcagga 1391

Qy   3331 GTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCGTTTTTTTTTGTTTAC 3390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 gtttctgcacagataccaggagctgctggatgacaaccaagctcgttttttttgtttac 1451

Qy   3391 GTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCAC 3450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 gtgtgcgatgcggtggctggctgtgcggctggacctcatcagcatcgccctcatcaccac 1511

Qy   3451 CACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGC 3510
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 cacggggctgatgatcgttcttatgcacgggcagattcccccagcctatgcgggtctcgc 1571

Qy   3511 CATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGA 3570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 catctcttatgctgtccagttaacggggctgttccagtttacggtcagactggcatctga 1631

Qy   3571 GACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTT 3630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 gacagaagctcgattcacctcggtggagaggatcaatcactacattaagactctgtcctt 1691

Qy   3631 GGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGA 3690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 ggaagcacctgccagaattaagaacaaggctccctcccctgactggccccaggagggaga 1751

Qy   3691 GGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAA 3750
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1752 ggtgacctttgagaacgcagagatgaggtaccgagaaaacctccctcttgtcctaaagaa 1811

Qy   3751 AGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGG 3810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1812 agtatccttcacgatcaaacctaaagagaagattggcattgtggggcggacaggatcagg 1871

Qy   3811 GAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAA 3870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1872 gaagtcctcgctggggatggccctcttccgtctggtggagttatctggaggctgcatcaa 1931

Qy   3871 GATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTAT 3930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1932 gattgatggagtgagaatcagtgatattggccttgccgacctccgaagcaaactctctat 1991

Qy   3931 CATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAA 3990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1992 cattcctcaagagccggtgctgttcagtggcactgtcagatcaaatttggacccccttcaa 2051

Qy   3991 CCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTAT 4050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2052 ccagtacactgaagaccagatttgggatgccctggagaggacacacatgaaagaatgtat 2111

Qy   4051 TGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGT 4110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2112 tgctcagctacctctgaaacttgaatctgaagtgatggagaatggggataacttctcagt 2171

Qy   4111 GGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGAT 4170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2172 gggggaacggcagctcttgtgcatagctagagccctgctccgccactgtaagattctgat 2231

Qy   4171 TTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCAT 4230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2232 tttagatgaagccacagctgccatggacacagagacagacttattgattcaagagaccat 2291

Qy   4231 CCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCT 4290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2292 ccgagaagcatttgcagactgtaccatgctgaccattgcccatcgcctgcacacggttct 2351

Qy   4291 AGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATC 4350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2352 aggctccgataggattatggtgctggcccagggacaggtggtggagtttgacaccccatc 2411

Qy   4351 GGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGCCATGTTTGCTGCTGCAGAGAACAA 4410
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2412 ggtccttctgtccaacgacagtt-ccgattctatgccatgtttgctgctgcagagaacaa 2470

Qy   4411 GGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGAAGTCTCTTTTCTTTAGAGCATTGC 4470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2471 ggtcgctgtcaagggctgactcctccctgttgacgaagtctcttttcttagagcattgc 2530

Qy   4471 CATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCCTCCTACCGAAACCTTGCCTTTCTC 4530
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2531 cattccctgcctggggcgggcccc-tcatcgcgtcctcctaccgaaaccttgcctttctc 2589

Qy   4531 GATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTTGTGTGTTTCACTTTTAGGGAGAGT 4590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 gattttatctttcgcacagcagttccggattggcttgtgtgtttcacttttagggagagt 2649

Qy   4591 CATATTTTGATTATTGTATTTATTCCATATTCATGTAAACAAAATTTAGTTTTTGTTCTT 4650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 catattttgattattgtatttattccatattcatgtaaacaaaatttagttttgttctt 2709

Qy   4651 AATTGCACTCTAAAAGGTTCAGGGAACCGTTATTATAATTGTATCAGAGGCCTATAATGA 4710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 aattgcactctaaaaggttcagggaaccgttattataattgtatcagaggcctataatga 2769

Qy   4711 AGCTTTATACGTGTAGCTATATCTATATATAATTCTGTACATAGCCTATATTTACAGTGA 4770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 agctttatacgtgtagctatatctatatataattctgtacatagcctatatttacagtga 2829

Qy   4771 AAATGTAAGCTGTTTATTTTATATTAAAATAAGCACTGTGCTAAAAAAA 4819
          |||||||||||||||||||||||||||||||||||||||||||| || |
Db   2830 aaatgtaagctgtttattttatattaaaataagcactgtgctaataaca 2878
```

Search completed: August 11, 2002, 11:01:58
Job time: 6288 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 09:18:35 ; Search time 627.48 Seconds
(without alignments)
18845.237 Million cell updates/sec

Title: US-09-528-031-1
Perfect score: 4847
Sequence: 1 GGCTCATGCTCGGGAGCGTG.....AAAAAAAAAAGGGCGGCCGC 4847

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1437365 seqs, 1219827628 residues

Total number of hits satisfying chosen parameters: 2874730

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4792.6	98.9	5838	5	US-09-647-140A-3	Sequence 3, Appli
2	4792.6	98.9	5838	7	US-10-007-926A-325	Sequence 325, App
3	4307.6	88.9	4314	7	US-10-154-452-1	Sequence 1, Appli
4	3929	81.1	3978	7	US-10-154-452-5	Sequence 5, Appli
5	3142	64.8	5881	7	US-10-172-086-81	Sequence 81, Appl
c 6	3011	62.1	5881	7	US-10-172-086-82	Sequence 82, Appl
7	768	15.8	4862	6	US-10-087-782A-1	Sequence 1, Appli
8	725.4	15.0	4083	7	US-10-162-012-35	Sequence 35, Appl
9	725.4	15.0	4638	7	US-10-162-012-33	Sequence 33, Appl
10	591.8	12.2	1579	7	US-10-137-337-228	Sequence 228, App
11	511.2	10.5	5011	1	PCT-US02-07787-35	Sequence 35, Appl
12	511.2	10.5	5011	5	US-09-442-384B-504	Sequence 504, App
13	437.4	9.0	4231	5	US-09-930-213-287	Sequence 287, App
14	437.4	9.0	4231	5	US-09-647-140A-1	Sequence 1, Appli
15	409.8	8.5	426	7	US-10-011-154-3846	Sequence 3846, Ap
16	401.4	8.3	457	5	US-09-918-995-28384	Sequence 28384, A
17	376.8	7.8	5099	6	US-10-191-803-60	Sequence 60, Appl
18	363.6	7.5	4977	1	PCT-US02-18947-472	Sequence 472, App
19	363.6	7.5	4977	7	US-10-172-118-472	Sequence 472, App
20	362.4	7.5	4509	5	US-09-647-140A-7	Sequence 7, Appli
21	356	7.3	5079	5	US-09-647-140A-5	Sequence 5, Appli
22	351.6	7.3	6628	6	US-10-191-803-61	Sequence 61, Appl
23	349.2	7.2	4869	5	US-09-935-625-26954	Sequence 26954, A
24	344.4	7.1	4869	5	US-09-935-625-26571	Sequence 26571, A
25	340.8	7.0	4896	5	US-09-935-625-3325	Sequence 3325, Ap
26	340.8	7.0	4896	5	US-09-935-625-26040	Sequence 26040, A
27	334.6	6.9	4872	5	US-09-935-625-3010	Sequence 3010, Ap
28	334.6	6.9	4872	5	US-09-935-625-25376	Sequence 25376, A
29	306.4	6.3	1981	5	US-09-919-002-2634	Sequence 2634, Ap
30	301.2	6.2	489	7	US-10-007-926A-324	Sequence 324, App
31	300.8	6.2	4551	5	US-09-935-625-5375	Sequence 5375, Ap
32	300.8	6.2	4551	5	US-09-935-625-8195	Sequence 8195, Ap
33	300.8	6.2	4551	5	US-09-935-625-20408	Sequence 20408, A
34	300.8	6.2	4551	5	US-09-935-625-25429	Sequence 25429, A
35	289.8	6.0	1110	6	US-10-198-717-7	Sequence 7, Appli
36	288.8	6.0	1098	6	US-10-198-717-4	Sequence 4, Appli
37	278.4	5.7	4369	5	US-09-935-625-7276	Sequence 7276, Ap
38	278.4	5.7	4369	5	US-09-935-625-16232	Sequence 16232, A
39	251.2	5.2	4566	5	US-09-935-625-5575	Sequence 5575, Ap
40	251.2	5.2	4566	5	US-09-935-625-8786	Sequence 8786, Ap
41	251.2	5.2	4566	5	US-09-935-625-21006	Sequence 21006, A
42	251.2	5.2	4566	5	US-09-935-625-25853	Sequence 25853, A
43	248	5.1	4548	8	US-60-360-039-25324	Sequence 25324, A
44	246.4	5.1	4524	8	US-60-360-039-27791	Sequence 27791, A
45	232.8	4.8	4338	8	US-60-360-039-25928	Sequence 25928, A

ALIGNMENTS

```
RESULT 1
US-09-647-140A-3
; Sequence 3, Application US/09647140A
; GENERAL INFORMATION:
;  APPLICANT: Fox Chase Cancer Center
;  APPLICANT:  Kruh, Gary D.
;  APPLICANT:  Lee, Kun
;  APPLICANT:  Belinsky, Martin G.
;  APPLICANT:  Bain, Lisa J.
;  TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
;  TITLE OF INVENTION:  Nucleic Acids and Methods of Use Thereof
;  FILE REFERENCE: FCCC 98-02
;  CURRENT APPLICATION NUMBER: US/09/647,140A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: PCT/US99/06644
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,759
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/095,153
;  PRIOR FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 5838
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-647-140A-3


  Query Match             98.9%;  Score 4792.6;  DB 5;  Length 5838;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4809;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy       1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 70

Qy      61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      71 gaattctgatgtgaaactaacagtctgtgagccctggaacctccgctcagagaagatgaa 130

Qy     121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 190

Qy     181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 250
```

```
Qy   241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
Db   251 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 310

Qy   301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
Db   311 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 370

Qy   361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
Db   371 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 430

Qy   421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
Db   431 caatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgtgtggc 490

Qy   481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
Db   491 ccacaagaaggggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 550

Qy   541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
Db   551 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 610

Qy   601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
Db   611 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 670

Qy   661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
Db   671 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 730

Qy   721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
Db   731 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 790

Qy   781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
Db   791 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 850

Qy   841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
Db   851 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 910

Qy   901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
Db   911 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 970

Qy   961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
Db   971 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1030

Qy  1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
Db  1031 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1090

Qy  1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
Db  1091 atcagctgtttttatcctcttttacccagcaatgatgtttgcatcacggctcacagcata 1150

Qy  1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
Db  1151 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1210

Qy  1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
Db  1211 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1270

Qy  1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
Db  1271 aaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggtatcac 1330

Qy  1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
Db  1331 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1390

Qy  1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
Db  1391 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1450

Qy  1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
Db  1451 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1510

Qy  1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
Db  1511 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1570

Qy  1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
Db  1571 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1630

Qy  1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
Db  1631 ccactccagtatccagaactcgcccaagctgaccccaaaatgaaaaaagacaagagggc 1690

Qy  1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
Db  1691 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1750

Qy  1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
Db  1751 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1810

Qy  1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
Db  1811 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1870

Qy  1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
Db  1871 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1930

Qy  1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
Db  1931 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 1990

Qy  1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
Db  1991 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2050

Qy  2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
Db  2051 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2110

Qy  2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
Db  2111 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2170

Qy  2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
Db  2171 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2230

Qy  2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
Db  2231 caggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggcaacca 2290

Qy  2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
Db  2291 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2350

Qy  2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
Db  2351 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2410

Qy  2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
```

```
Db   2411 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2470
Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
Db   2471 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2530
Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
Db   2531 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2590
Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
Db   2591 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2650
Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
Db   2651 ctggtcagtatatggtgtctacatccaggctgctgggggcccctggcattcctggttat 2710
Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
Db   2711 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2770
Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
Db   2771 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2830
Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
Db   2831 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2890
Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
Db   2891 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 2950
Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
Db   2951 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3010
Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
Db   3011 ttttgacacgaccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3070
Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
Db   3071 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3130
Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
Db   3131 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3190
Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
Db   3191 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3250
Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
Db   3251 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3310
Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
Db   3311 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3370
Qy   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
Db   3371 tgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3430
Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
Db   3431 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3490
Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
Db   3491 gcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3550
Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
Db   3551 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3610
Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
Db   3611 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3670
Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
Db   3671 tccctccccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3730
Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Db   3731 ccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3790
Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Db   3791 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3850
Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Db   3851 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3910
Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Db   3911 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 3970
Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Db   3971 cactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgggatgc 4030
Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
Db   4031 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4090
Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
Db   4091 agtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcatagctag 4150
Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
Db   4151 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4210
Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
Db   4211 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4270
Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
Db   4271 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4330
Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
Db   4331 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4390
Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
Db   4391 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4450
Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
Db   4451 tgacgaagtctcttttcttagagcattgccattccctgcctggggcgggcccc-tcatc 4509
Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
Db   4510 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4569
Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
Db   4570 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4629
```

```
Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4630 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4689

Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4690 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4749

Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4750 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttattttatattaaaat 4809

Qy   4801 AAGCACTGTGCTAAAAAAA 4819
          ||||||||||||||| || |
Db   4810 aagcactgtgctaataaca 4828


RESULT   2
US-10-007-926A-325
; Sequence 325, Application US/10007926A
; GENERAL INFORMATION:
;  APPLICANT: BERTUCCI, FRANCOIS
;  APPLICANT:  HOULGATTE, REMI
;  APPLICANT:  BIRNBAUM, DANIEL
;  APPLICANT:  NGUYEN, CATHERINE
;  APPLICANT:  VIENS, PATRICE
;  APPLICANT:  FERT, VINCENT
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
;  TITLE OF INVENTION:  USING ARRAYS OF CANDIDATE GENES
;  FILE REFERENCE: 1546-R-00
;  CURRENT APPLICATION NUMBER: US/10/007,926A
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 60/254,090
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 468
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 325
;   LENGTH: 5838
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: atp-binding cassette, sub-family c
;   OTHER INFORMATION: (cftr/mrp), member 5 (ABCC5) gene.
US-10-007-926A-325


  Query Match             98.9%;  Score 4792.6;  DB 7;  Length 5838;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4809;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy      1 GGCTCATGCTCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 ggctcatgctcgggagcgtggttgagcggctggcgcggttgtcctggagcaggggcgcag 70

Qy     61 GAATTCTGATGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     71 gaattctgatgtgaaactaacagtctgtgagccctggaacctccgctcagagaagatgaa 130

Qy    121 GGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 ggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtgaggga 190

Qy    181 GAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 gagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggagaactcg 250

Qy    241 ACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 accgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctctcttga 310

Qy    301 TGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 tgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaagtacca 370

Qy    361 TCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGA 420
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    371 tcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcacccagtgga 430

Qy    421 CAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 caatgctgggctttttcctgtatgacttttcgtggctttcttctctggcccgtgtggc 490

Qy    481 CCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 ccacaagaaggggggagctctcaatggaagacgtgtggtctctgtccaagcacgagtcttc 550

Qy    541 TGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 tgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagttgggcc 610

Qy    601 AGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 agacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatcctgtc 670

Qy    661 CATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 catcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatggtgaa 730

Qy    721 ACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    731 acacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttgttagt 790

Qy    781 GCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 gctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgggcatt 850

Qy    841 GAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 gaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaagaagat 910

Qy    901 CCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 ccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgctccaa 970

Qy    961 CGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 cgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggaggacccgt 1030

Qy   1021 TGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 tgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttcctggg 1090

Qy   1081 ATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1091 atcagctgtttttatcctcttttacccagcaatgatgtttgcatcacggctcacagcata 1150

Qy   1141 TTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1151 tttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaagttct 1210

Qy   1201 TACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1211 tacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagtgttca 1270

Qy   1261 GAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCAC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||| | |||||
Db   1271 aaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagggtatcac 1330

Qy   1321 TGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATAT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 tgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgttcatat 1390

Qy   1381 GACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1391 gaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttcaattc 1450
```

```
Qy   1441 CATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1451 catgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcctcagt 1510

Qy   1501 GGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1511 ggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaagaacaa 1570

Qy   1561 ACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1571 accagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggactcctc 1630

Qy   1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1631 ccactccagtatccagaactcgcccaagctgaccccaaaatgaaaaaagacaagagggc 1690

Qy   1681 TTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1691 ttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcggtgct 1750

Qy   1741 GGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1751 ggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaagagga 1810

Qy   1801 AGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1811 agaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagcatcga 1870

Qy   1861 TCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAAC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1871 tctggagatccaagagggtaaactggttggaatctgcggcagtgtgggaagtggaaaaac 1930

Qy   1921 CTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1931 ctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgcaatcag 1990

Qy   1981 TGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1991 tggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgagagacaa 2050

Qy   2041 CATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2051 catcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagctgctg 2110

Qy   2101 CCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2111 cctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagagcgagg 2170

Qy   2161 AGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2171 agccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtatagtga 2230

Qy   2221 CAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2231 caggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggcaacca 2290

Qy   2281 CATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 catcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgttaccca 2350

Qy   2341 CCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTAC 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2351 ccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgtattac 2410

Qy   2401 GGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2411 ggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatttttaa 2470

Qy   2461 TAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2471 taacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaaccagtgg 2530

Qy   2521 TTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2531 ttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaaaaagc 2590

Qy   2581 AGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2591 agtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttcagtgcc 2650

Qy   2641 CTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTAT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2651 ctggtcagtatatggtgtctacatccaggctgctgggggcccctggcattcctggttat 2710

Qy   2701 TATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTA 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2711 tatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttgagtta 2770

Qy   2761 CTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2771 ctggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcggtgag 2830

Qy   2821 TGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2831 tgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctctccat 2890

Qy   2881 GGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 ggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacgctgcg 2950

Qy   2941 AGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 agcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatgaagtt 3010

Qy   3001 TTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3011 ttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggatgaagt 3070

Qy   3061 TGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3071 tgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtgttctt 3130

Qy   3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3131 ctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccccttgt 3190

Qy   3181 CATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3191 catcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaagcgtct 3250

Qy   3241 GGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGC 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3251 ggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggccttgc 3310

Qy   3301 CACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3311 caccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctgctgga 3370

Qy   3361 TGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCT 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3371 tgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtgcggct 3430

Qy   3421 GGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3431 ggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatgcacgg 3490

Qy   3481 GCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3491 gcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacggggct 3550

Qy   3541 GTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3551 gttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtggagag 3610

Qy   3601 GATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGC 3660
```

```
Db   3611 gatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaacaaggc 3670
Qy   3661 TCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTA 3720
Db   3671 tccctcccctgactggccccaggagggagaggtgacctttgagaacgcagagatgaggta 3730
Qy   3721 CCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAA 3780
Db   3731 ccgagaaaacctccctcttgtcctaaagaaagtatccttcacgatcaaacctaaagagaa 3790
Qy   3781 GATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCG 3840
Db   3791 gattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctcttccg 3850
Qy   3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGG 3900
Db   3851 tctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgatattgg 3910
Qy   3901 CCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGG 3960
Db   3911 ccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttcagtgg 3970
Qy   3961 CACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC 4020
Db   3971 cactgtcagatcaaatttggacccctcaaccagtacactgaagaccagatttgggatgc 4030
Qy   4021 CCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGA 4080
Db   4031 cctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaatctga 4090
Qy   4081 AGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAG 4140
Db   4091 agtgatggagaatggggataacttctcagtggggaacggcagctcttgtgcatagctag 4150
Qy   4141 AGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4200
Db   4151 agccctgctccgccactgtaagattctgattttagatgaagccacagctgccatggacac 4210
Qy   4201 AGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCT 4260
Db   4211 agagacagacttattgattcaagagaccatccgagaagcatttgcagactgtaccatgct 4270
Qy   4261 GACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCA 4320
Db   4271 gaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctggccca 4330
Qy   4321 GGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATT 4380
Db   4331 gggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcccgatt 4390
Qy   4381 CTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGT 4440
Db   4391 ctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgt 4450
Qy   4441 TGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATC 4500
Db   4451 tgacgaagtctcttttcttagagcattgccattccctgcctggggcgggcccc-tcatc 4509
Qy   4501 GCGTCCTCCTACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGAT 4560
Db   4510 gcgtcctcctaccgaaaccttgcctttctcgattttatctttcgcacagcagttccggat 4569
Qy   4561 TGGCTTGTGTGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATAT 4620
Db   4570 tggcttgtgtgtttcacttttagggagagtcatattttgattattgtatttattccatat 4629
Qy   4621 TCATGTAAACAAAATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGT 4680
Db   4630 tcatgtaaacaaaatttagtttttgttcttaattgcactctaaaaggttcagggaaccgt 4689
Qy   4681 TATTATAATTGTATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATAT 4740
Db   4690 tattataattgtatcagaggcctataatgaagctttatacgtgtagctatatctatatat 4749
Qy   4741 AATTCTGTACATAGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAAT 4800
Db   4750 aattctgtacatagcctatatttacagtgaaaatgtaagctgtttattttatattaaaat 4809
Qy   4801 AAGCACTGTGCTAAAAAAA 4819
Db   4810 aagcactgtgctaataaca 4828
```

```
RESULT   3
US-10-154-452-1
; Sequence 1, Application US/10154452
; GENERAL INFORMATION:
;  APPLICANT: Reiner, Peter B.
;  APPLICANT:  Roy, Josee
;  APPLICANT:  Connop, Bruce P.
;  TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
;  TITLE OF INVENTION:  EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
;  TITLE OF INVENTION:  DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
;  FILE REFERENCE: 100103.420
;  CURRENT APPLICATION NUMBER: US/10/154,452
;  CURRENT FILING DATE:  2002-05-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 4314
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-154-452-1
```

Query Match 88.9%; Score 4307.6; DB 7; Length 4314;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4310; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy    116 ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG 175
Db      1 atggaggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtg 60
Qy    176 AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA 235
Db     61 agggagagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggaga 120
Qy    236 ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT 295
Db    121 actcgaccgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctct 180
Qy    296 CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG 355
Db    181 cttgatgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaag 240
Qy    356 TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCA 415
Db    241 taccatcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcaccca 300
Qy    416 GTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGT 475
Db    301 gtggacaatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgt 360
Qy    476 GTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG 535
Db    361 gtggcccacaagaaggggggagctctcaatggaagacgtgtggtctctgtccaagcacgag 420
Qy    536 TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT 595
Db    421 tcttctgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagtt 480
Qy    596 GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC 655
Db    481 gggccagacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatc 540
```

```
Qy    656 CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ctgtccatcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatg 600

Qy    716 GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtgaaacacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttg 660

Qy    776 TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ttagtgctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgg 720

Qy    836 GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAAGCATGGCATTTAAG 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gcattgaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaag 780

Qy    896 AAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 aagatccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgc 840

Qy    956 TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA 1015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tccaacgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggagga 900

Qy   1016 CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC 1075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 cccgttgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttc 960

Qy   1076 CTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA 1135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ctgggatcagctgtttttatcctctttacccagcaatgatgtttgcatcacggctcaca 1020

Qy   1136 GCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 gcatatttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaa 1080

Qy   1196 GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT 1255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 gttcttacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagt 1140

Qy   1256 GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGC 1315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gttcagaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagagc 1200

Qy   1316 ATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT 1375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 atcactgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgtt 1260

Qy   1376 CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTC 1435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 catatgaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttc 1320

Qy   1436 AATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCC 1495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aattccatgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcc 1380

Qy   1496 TCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAG 1555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 tcagtggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaag 1440

Qy   1556 AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC 1615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 aacaaaccagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggac 1500

Qy   1616 TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG 1675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 tcctcccactccagtatccagaactcgcccaagctgaccccaaaatgaaaaaagacaag 1560

Qy   1676 AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG 1735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 agggcttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcg 1620

Qy   1736 GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAA 1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 gtgctggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaa 1680

Qy   1796 GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC 1855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 gaggaagaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagc 1740

Qy   1856 ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA 1915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 atcgatctggagatccaagagggtaaactggttggaatctgtggcagtgtgggaagtgga 1800

Qy   1916 AAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA 1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 aaaacctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgca 1860

Qy   1976 ATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA 2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 atcagtggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgaga 1920

Qy   2036 GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGC 2095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 gacaacatcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagc 1980

Qy   2096 TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAG 2155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 tgctgcctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagag 2040

Qy   2156 CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTAT 2215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 cgaggagccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtat 2100

Qy   2216 AGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGC 2275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 agtgacaggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggc 2160

Qy   2276 AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT 2335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 aaccacatcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgtt 2220

Qy   2336 ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT 2395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 acccaccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgt 2280

Qy   2396 ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT 2455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 attacggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatt 2340

Qy   2456 TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC 2515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 tttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaacc 2400

Qy   2516 AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAA 2575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 agtggttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaa 2460

Qy   2576 AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA 2635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 aaagcagtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttca 2520

Qy   2636 GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTG 2695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 gtgccctggtcagtatatggtgtctacatccaggctgctgggggcccctggcattcctg 2580

Qy   2696 GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG 2755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 gttattatggccctttcatgctgaatgtaggcagcaccgccttcagcacctggtggttg 2640

Qy   2756 AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG 2815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 agttactggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcg 2700

Qy   2816 GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC 2875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    2701 gtgagtgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctc 2760
Qy    2876 TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG 2935
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 tccatggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacg 2820

Qy    2936 CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG 2995
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 ctgcgagcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatg 2880

Qy    2996 AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT 3055
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 aagtttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggat 2940

Qy    3056 GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTG 3115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 gaagttgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtg 3000

Qy    3116 TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC 3175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 ttcttctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccc 3060

Qy    3176 CTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAG 3235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 cttgtcatcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaag 3120

Qy    3236 CGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGC 3295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 cgtctggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggc 3180

Qy    3296 CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG 3355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 cttgccaccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctg 3240

Qy    3356 CTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTG 3415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 ctggatgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtg 3300

Qy    3416 CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG 3475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 cggctggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatg 3360

Qy    3476 CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG 3535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 cacgggcagattcccccagcctatgcgggtctcgccatctcttatgctgtccagttaacg 3420

Qy    3536 GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTG 3595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 gggctgttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtg 3480

Qy    3596 GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC 3655
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 gagaggatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaac 3540

Qy    3656 AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG 3715
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 aaggctccctccccctgactggccccaggagggagaggtgacctttgagaacgcagagatg 3600

Qy    3716 AGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA 3775
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 aggtaccgagaaaacctccctctcgtcctaaagaaagtatccttcacgatcaaacctaaa 3660

Qy    3776 GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC 3835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 gagaagattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctc 3720

Qy    3836 TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT 3895
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 ttccgtctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgat 3780

Qy    3896 ATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTC 3955
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 attggccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttc 3840
```

```
Qy    3956 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG 4015
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 agtggcactgtcagatcaaatttggacccccttcaaccagtacactgaagaccagatttgg 3900

Qy    4016 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA 4075
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 gatgccctggagaggacacacatgaaagaatgtattgctcagctacctctgaaacttgaa 3960

Qy    4076 TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA 4135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 tctgaagtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgcata 4020

Qy    4136 GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG 4195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 gctagagccctgctccgccactgtaagattctgattttagatgaagccacagctgccatg 4080

Qy    4196 GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACC 4255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 gacacagagacagacttattgattcaagagaccatccgagaagcatttgcagactgtacc 4140

Qy    4256 ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG 4315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4141 atgctgaccattgcccatcgcctgcacacggttctaggctccgataggattatggtgctg 4200

Qy    4316 GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC 4375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4201 gcccagggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagttcc 4260

Qy    4376 CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA 4429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 cgattctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctga 4314
```

RESULT 4
US-10-154-452-5
; Sequence 5, Application US/10154452
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Roy, Josee
; APPLICANT: Connop, Bruce P.
; TITLE OF INVENTION: INCREASED FUNCTIONAL ACTIVITY AND/OR
; TITLE OF INVENTION: EXPRESSION OF ABC TRANSPORTERS PROTECTS AGAINST THE LOSS OF
; TITLE OF INVENTION: DOPAMINE NEURONS ASSOCIATED WITH PARKINSON'S DISEASE
; FILE REFERENCE: 100103.420
; CURRENT APPLICATION NUMBER: US/10/154,452
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3978
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-154-452-5

Query Match 81.1%; Score 3929; DB 7; Length 3978;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3932; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy     116 ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG 175
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 atggaggatatcgacataggaaaagagtatatcatccccagtcctgggtatagaagtgtg 60

Qy     176 AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA 235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 agggagagaaccagcacttctgggacgcacagagaccgtgaagattccaagttcaggaga 120

Qy     236 ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT 295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 actcgaccgttggaatgccaagatgccttggaaacagcagcccgagccgagggcctctct 180

Qy     296 CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG 355
```

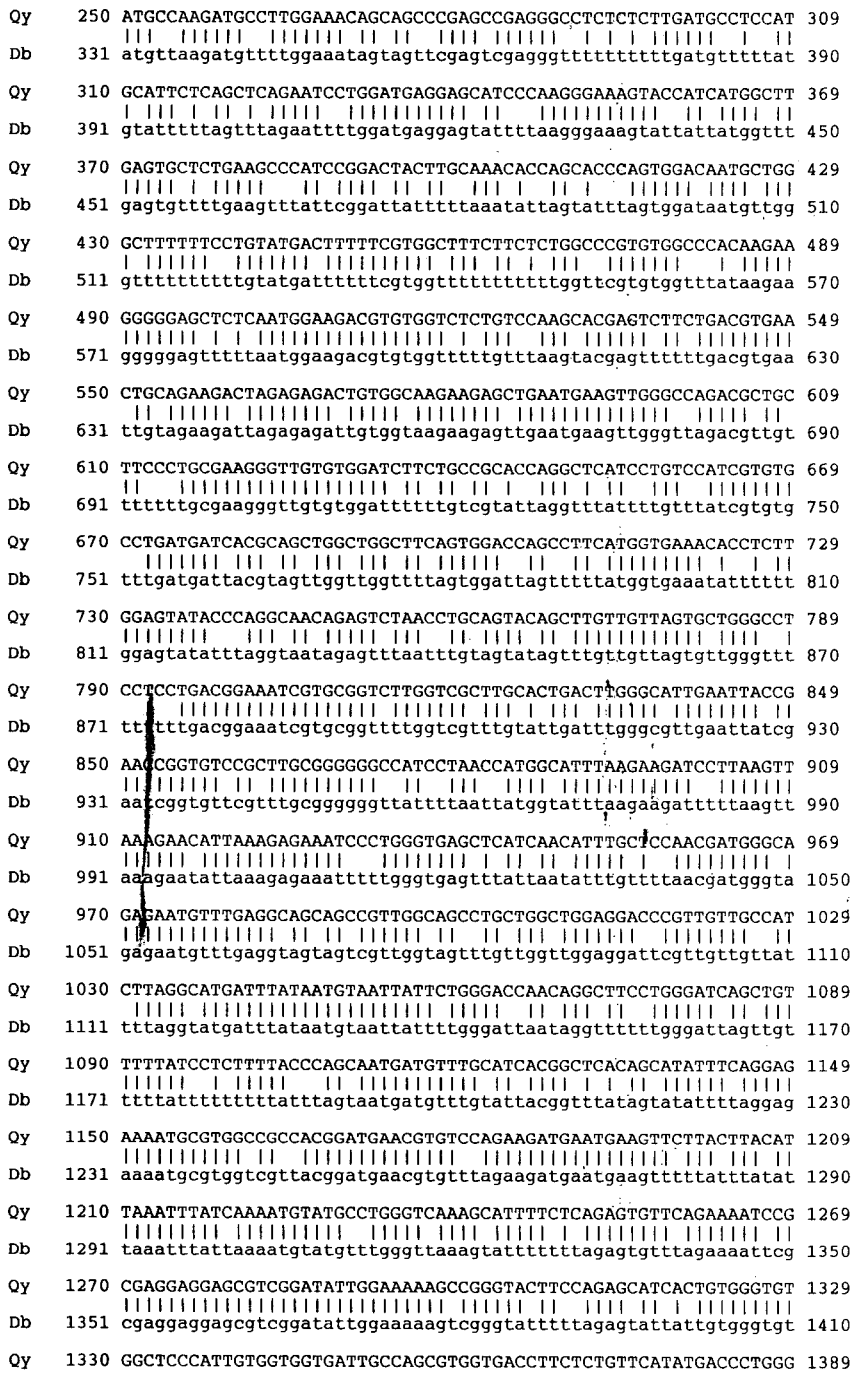
```
Db    181 cttgatgcctccatgcattctcagctcagaatcctggatgaggagcatcccaagggaaag 240
Qy    356 TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCA 415
Db    241 taccatcatggcttgagtgctctgaagcccatccggactacttccaaacaccagcaccca 300
Qy    416 GTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGT 475
Db    301 gtggacaatgctgggctttttttcctgtatgacttttttcgtggctttcttctctggcccgt 360
Qy    476 GTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG 535
Db    361 gtggcccacaagaaggggagctctcaatggaagacgtgtggtctctgtccaagcacgag 420
Qy    536 TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT 595
Db    421 tcttctgacgtgaactgcagaagactagagagactgtggcaagaagagctgaatgaagtt 480
Qy    596 GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC 655
Db    481 gggccagacgctgcttccctgcgaagggttgtgtggatcttctgccgcaccaggctcatc 540
Qy    656 CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG 715
Db    541 ctgtccatcgtgtgcctgatgatcacgcagctggctggcttcagtggaccagccttcatg 600
Qy    716 GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG 775
Db    601 gtgaaacacctcttggagtatacccaggcaacagagtctaacctgcagtacagcttgttg 660
Qy    776 TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG 835
Db    661 ttagtgctgggcctcctcctgacggaaatcgtgcggtcttggtcgcttgcactgacttgg 720
Qy    836 GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG 895
Db    721 gcattgaattaccgaaccggtgtccgcttgcgggggccatcctaaccatggcatttaag 780
Qy    896 AAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC 955
Db    781 aagatccttaagttaaagaacattaaagagaaatccctgggtgagctcatcaacatttgc 840
Qy    956 TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA 1015
Db    841 tccaacgatgggcagagaatgtttgaggcagcagccgttggcagcctgctggctggagga 900
Qy   1016 CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC 1075
Db    901 cccgttgttgccatcttaggcatgatttataatgtaattattctgggaccaacaggcttc 960
Qy   1076 CTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA 1135
Db    961 ctgggatcagctgtttttatcctctttttacccagcaatgatgtttgcatcacggctcaca 1020
Qy   1136 GCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA 1195
Db   1021 gcatatttcaggagaaaatgcgtggccgccacggatgaacgtgtccagaagatgaatgaa 1080
Qy   1196 GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT 1255
Db   1081 gttcttacttacattaaatttatcaaaatgtatgcctgggtcaaagcattttctcagagt 1140
Qy   1256 GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGC 1315
Db   1141 gttcagaaaatccgcgaggaggagcgtcggatattggaaaaagccgggtacttccagagc 1200
Qy   1316 ATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT 1375
Db   1201 atcactgtgggtgtggctcccattgtggtggtgattgccagcgtggtgaccttctctgtt 1260
Qy   1376 CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTC 1435
Db   1261 catatgaccctgggcttcgatctgacagcagcacaggctttcacagtggtgacagtcttc 1320
Qy   1436 AATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCC 1495
Db   1321 aattccatgacttttgctttgaaagtaacaccgttttcagtaaagtccctctcagaagcc 1380
Qy   1496 TCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAG 1555
Db   1381 tcagtggctgttgacagatttaagagtttgtttctaatggaagaggttcacatgataaag 1440
Qy   1556 AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC 1615
Db   1441 aacaaaccagccagtcctcacatcaagatagagatgaaaaatgccaccttggcatgggac 1500
Qy   1616 TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG 1675
Db   1501 tcctcccactccagtatccagaactcgcccaagctgacccccaaaatgaaaaaagacaag 1560
Qy   1676 AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG 1735
Db   1561 agggcttccaggggcaagaaagagaaggtgaggcagctgcagcgcactgagcatcaggcg 1620
Qy   1736 GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAA 1795
Db   1621 gtgctggcagagcagaaaggccacctcctcctggacagtgacgagcggcccagtcccgaa 1680
Qy   1796 GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC 1855
Db   1681 gaggaagaaggcaagcacatccacctgggccacctgcgcttacagaggacactgcacagc 1740
Qy   1856 ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA 1915
Db   1741 atcgatctggagatccaagagggtaaactggttggaatctgtggcagtgtgggaagtgga 1800
Qy   1916 AAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA 1975
Db   1801 aaaacctctctcatttcagccattttaggccagatgacgcttctagagggcagcattgca 1860
Qy   1976 ATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA 2035
Db   1861 atcagtggaaccttcgcttatgtggcccagcaggcctggatcctcaatgctactctgaga 1920
Qy   2036 GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGC 2095
Db   1921 gacaacatcctgtttgggaaggaatatgatgaagaaagatacaactctgtgctgaacagc 1980
Qy   2096 TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAG 2155
Db   1981 tgctgcctgaggcctgacctggccattcttcccagcagcgacctgacggagattggagag 2040
Qy   2156 CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTAT 2215
Db   2041 cgaggagccaacctgagcggtgggcagcgccagaggatcagccttgcccgggccttgtat 2100
Qy   2216 AGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGC 2275
Db   2101 agtgacaggagcatctacatcctggacgacccccctcagtgccttagatgcccatgtgggc 2160
Qy   2276 AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT 2335
Db   2161 aaccacatcttcaatagtgctatccggaaacatctcaagtccaagacagttctgtttgtt 2220
Qy   2336 ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT 2395
Db   2221 acccaccagttacagtacctggttgactgtgatgaagtgatcttcatgaaagagggctgt 2280
Qy   2396 ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT 2455
Db   2281 attacggaaagaggcacccatgaggaactgatgaatttaaatggtgactatgctaccatt 2340
Qy   2456 TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC 2515
Db   2341 tttaataacctgttgctgggagagacaccgccagttgagatcaattcaaaaaaggaaacc 2400
```

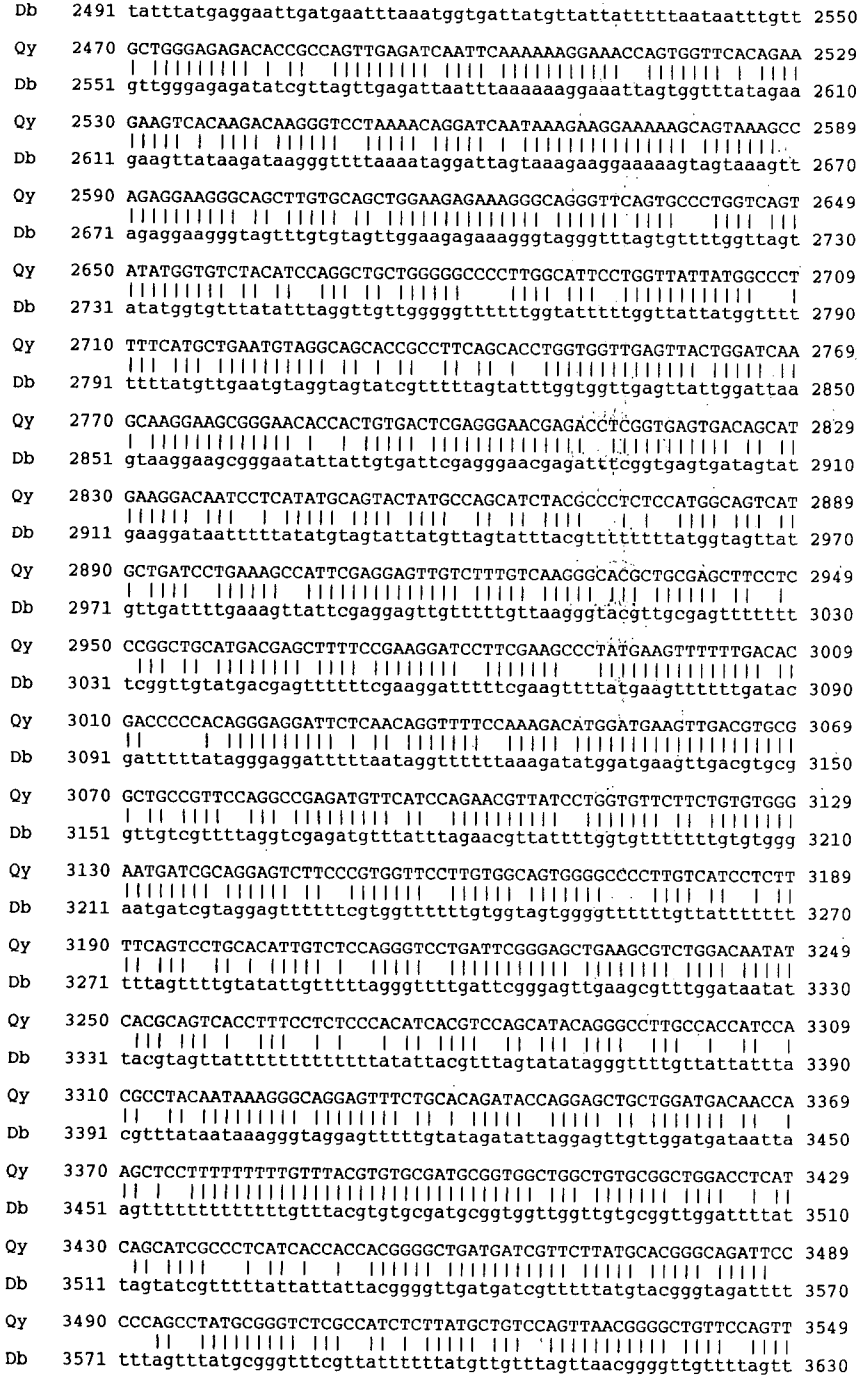
```
Qy   2516 AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAA 2575
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   2401 agtggttcacagaagaagtcacaagacaagggtcctaaaacaggatcagtaaagaaggaa 2460

Qy   2576 AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA 2635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 aaagcagtaaagccagaggaagggcagcttgtgcagctggaagagaaagggcagggttca 2520

Qy   2636 GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTG 2695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 gtgccctggtcagtatatggtgtctacatccaggctgctgggggcccCttggcattcctg 2580

Qy   2696 GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG 2755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 gttattatggccctttTcatgctgaatgtaggcagcaccgccttcagcacctggtggttg 2640

Qy   2756 AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGCGAACGAGACCTCG 2815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 agttactggatcaagcaaggaagcgggaacaccactgtgactcgagggaacgagacctcg 2700

Qy   2816 GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC 2875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 gtgagtgacagcatgaaggacaatcctcatatgcagtactatgccagcatctacgccctc 2760

Qy   2876 TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG 2935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 tccatggcagtcatgctgatcctgaaagccattcgaggagttgtctttgtcaagggcacg 2820

Qy   2936 CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG 2995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 ctgcgagcttcctcccggctgcatgacgagcttttccgaaggatccttcgaagccctatg 2880

Qy   2996 AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT 3055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 aagtttttgacacgacccccacagggaggattctcaacaggttttccaaagacatggat 2940

Qy   3056 GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTG 3115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 gaagttgacgtgcggctgccgttccaggccgagatgttcatccagaacgttatcctggtg 3000

Qy   3116 TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC 3175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ttcttctgtgtgggaatgatcgcaggagtcttcccgtggttccttgtggcagtggggccc 3060

Qy   3176 CTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAG 3235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 cttgtcatcctcttttcagtcctgcacattgtctccagggtcctgattcgggagctgaag 3120

Qy   3236 CGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGC 3295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 cgtctggacaatatcacgcagtcacctttcctctcccacatcacgtccagcatacagggc 3180

Qy   3296 CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG 3355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 cttgccaccatccacgcctacaataaagggcaggagtttctgcacagataccaggagctg 3240

Qy   3356 CTGGATGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTG 3415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 ctggatgacaaccaagctccttttttttttgtttacgtgtgcgatgcggtggctggctgtg 3300

Qy   3416 CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG 3475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 cggctggacctcatcagcatcgccctcatcaccaccacggggctgatgatcgttcttatg 3360

Qy   3476 CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG 3535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 cacgggcagattccccCagcctatgcgggtctcgccatctcttatgctgtccagttaacg 3420

Qy   3536 GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTG 3595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 gggctgttccagtttacggtcagactggcatctgagacagaagctcgattcacctcggtg 3480

Qy   3596 GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC 3655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 gagaggatcaatcactacattaagactctgtccttggaagcacctgccagaattaagaac 3540

Qy   3656 AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG 3715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 aaggctccctcccctgactggccccaggagggagaggtgacctttgagaacgcagagatg 3600

Qy   3716 AGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA 3775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 aggtaccgagaaaacctccctctcgtcctaaagaaagtatccttcacgatcaaacctaaa 3660

Qy   3776 GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC 3835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 gagaagattggcattgtggggcggacaggatcagggaagtcctcgctggggatggccctc 3720

Qy   3836 TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT 3895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 ttccgtctggtggagttatctggaggctgcatcaagattgatggagtgagaatcagtgat 3780

Qy   3896 ATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTC 3955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 attggccttgccgacctccgaagcaaactctctatcattcctcaagagccggtgctgttc 3840

Qy   3956 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG 4015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 agtggcactgtcagatcaaatttggacccCttcaaccagtacactgaagaccagatttgg 3900

Qy   4016 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTG 4052
          |||||||||||||||||||||||||||||||||| |
Db   3901 gatgccctggagaggacacacatgaaagaatgtatcg 3937
```

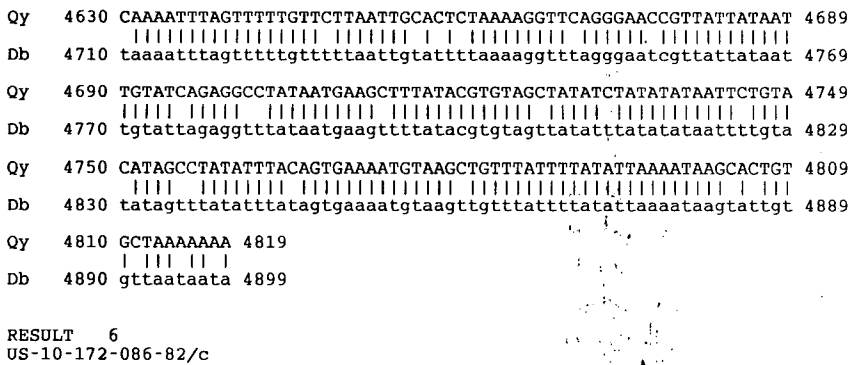
RESULT 5
US-10-172-086-81
; Sequence 81, Application US/10172086
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the differentiation
; TITLE OF INVENTION: of prostate tumors
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/172,086
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 81
; LENGTH: 5881
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-81

Query Match 64.8%; Score 3142; DB 7; Length 5881;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 3774; Conservative 0; Mismatches 1035; Indels 1; Gaps 1;

```
Qy     10 TCGGGAGCGTGGTTGAGCGGCTGGCGCGGTTGTCCTGGAGCAGGGGCGCAGGAATTCTGA 69
          |||||||||||||||||| |||||||||||  ||||| ||||||| ||||||| |||
Db     91 tcgggagcgtggttgagcggttggcgcggttgttttggagtaggggcgtaggaatttga 150

Qy     70 TGTGAAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAAGGATATCGA 129
          ||||||| ||| ||| ||||||   |||||  |  | | ||||||||||||||||||||
Db    151 tgtgaaattaatagtttgtgagttttggaatttttatttagagaagatgaaggatatcga 210

Qy    130 CATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTGAGGGAGAGAACCAG 189
          |||||||||||||||||  ||    |||  ||||||||||||||||||||||||||  ||
Db    211 tataggaaaagagtatattatttttagttttgggtatagaagtgtgagggagagaattag 270

Qy    190 CACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTCGACCGTTGGA 249
          | || ||||||| | ||||| |||||||||  ||||| ||||||| |||| |||||||
Db    271 tatttttgggacgtatagagatcgtgaagattttaagtttaggagaattcgatcgttgga 330
```

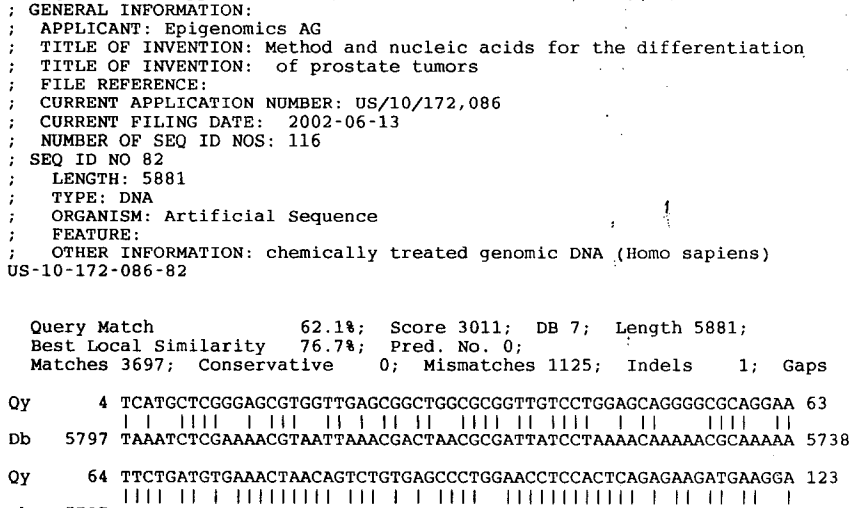

Qy 250 ATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCTCTTGATGCCTCCAT 309
Db 331 atgttaagatgttttggaaatagtagttcgagtcgagggttttttttttgatgtttttat 390
Qy 310 GCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAGTACCATCATGGCTT 369
Db 391 gtatttttagtttagaattttggatgaggagtattttaagggaaagtattattatggttt 450
Qy 370 GAGTGCTCTGAAGCCCATCCGGACTACTTGCAAACACCAGCACCCAGTGGACAATGCTGG 429
Db 451 gagtgttttgaagtttattcggattatttttaaatattagtatttagtggataatgttgg 510
Qy 430 GCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGTGTGGCCCACAAGAA 489
Db 511 gttttttttttgtatgatttttcgtggttttttttttggttcgtgtggtttataagaa 570
Qy 490 GGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAGTCTTCTGACGTGAA 549
Db 571 gggggagtttttaatggaagacgtgtggtttttgtttaagtacgagtttttgacgtgaa 630
Qy 550 CTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTTGGGCCAGACGCTGC 609
Db 631 ttgtagaagattagagagattgtggtaagaagagttgaatgaagttgggttagacgttgt 690
Qy 610 TTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATCCTGTCCATCGTGTG 669
Db 691 ttttttgcgaagggttgtgtggatttttgtcgtattaggtttatttgtttatcgtgtg 750
Qy 670 CCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATGGTGAAACACCTCTT 729
Db 751 tttgatgattacgtagttggttggttttagtggattagtttttatggtgaaatatttttt 810
Qy 730 GGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGGCCT 789
Db 811 ggagtatatttaggtaatagagtttaatttgtagtatagtttgttgttagtgttgggttt 870
Qy 790 CCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTACCG 849
Db 871 ttttttgacggaaatcgtgcggttttggtcgtttgtattgatttgggcgttgaattatcg 930
Qy 850 AACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTTAAGTT 909
Db 931 aatcggtgttcgtttgcgggggggttattttaattatggtatttaagaagatttttaagtt 990
Qy 910 AAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACGATGGGCA 969
Db 991 aaagaatattaaagagaaatttttgggtgagtttattaatatttgttttaacgatgggta 1050
Qy 970 GAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCCGTTGTTGCCAT 1029
Db 1051 gagaatgtttgaggtagtagtcgttggtagtttgttggttggaggattcgttgttgttat 1110
Qy 1030 CTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTCCTGGGATCAGCTGT 1089
Db 1111 tttaggtatgatttataatgtaattattttgggattaataggttttttgggattagttgt 1170
Qy 1090 TTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCATATTTCAGGAG 1149
Db 1171 ttttatttttttttatttagtaatgatgtttgtattacggtttatagtatattttaggag 1230
Qy 1150 AAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTTCTTACTTACAT 1209
Db 1231 aaaatgcgtggtcgttacggatgaacgtgtttagaagatgaatgaagtttttatttatat 1290
Qy 1210 TAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAATCCG 1269
Db 1291 taaatttattaaaatgtatgtttgggttaaagtatttttttagagtgtttagaaaattcg 1350
Qy 1270 CGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGGTGT 1329
Db 1351 cgaggaggagcgtcggatattggaaaaagtcgggtatttttagagtattattgtgggtgt 1410
Qy 1330 GGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTTCATATGACCCTGGG 1389
Db 1411 ggtttttattgtggtggtgattgttagcgtggtgatttttttgtttatatgattttggg 1470
Qy 1390 CTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTCAATTCCATGACTTT 1449
Db 1471 tttcgatttgatagtagtataggtttttatagtggtgatagtttttaattttatgatttt 1530
Qy 1450 TGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCCTCAGTGGCTGTTGA 1509
Db 1531 tgttttgaaagtaatatcgtttttagtaaagttttttttagaagttttagtggttgttga 1590
Qy 1510 CAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAGAACAAACCAGCCAG 1569
Db 1591 tagatttaagagtttgtttttaatggaagaggtttatatgataaagaataaattagttag 1650
Qy 1570 TCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGACTCCTCCCACTCCAG 1629
Db 1651 tttttatattaagatagagatgaaaaatgttattttggtatgggatttttttattttag 1710
Qy 1630 TATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTCCAGGGG 1689
Db 1711 tatttagaattcgtttaagttgatttttaaaatgaaaaaagataagagggtttttagggg 1770
Qy 1690 CAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGCAGAGCA 1749
Db 1771 taagaaagagaaggtgaggtagttgtagcgtattgagtattaggcggtgttggtagagta 1830
Qy 1750 GAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGAAGGCAA 1809
Db 1831 gaaaggttatttttttttggatagtgacgagcggtttagtttcgaagaggaagaaggtaa 1890
Qy 1810 GCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGAT 1869
Db 1891 gtatatttatttgggttatttgcgtttatagaggatattgtatagcgtcgatttggagat 1950
Qy 1870 CCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCAT 1929
Db 1951 ttaagagggtaaattggttggaatttgcggtagtgtgggaagtggaaaaatttttttttat 2010
Qy 1930 TTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTT 1989
Db 2011 tttagttattttaggttagatgacgtttttagagggtagtattgtaattagtggaatttt 2070
Qy 1990 CGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTT 2049
Db 2071 cgtttatgtggtttagtaggtttggatttttaatgttattttgagagataatattttgtt 2130
Qy 2050 TGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCC 2109
Db 2131 tgggaaggaatatgatgaagaaagatataatttttgtgttgaatagttgttgtttgaggtt 2190
Qy 2110 TGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCT 2169
Db 2191 tgatttggttatttttttagtagcgatttgacggagattggagagcgaggagttaattt 2250
Qy 2170 GAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCAT 2229
Db 2251 gagcggtgggtagcgttagaggattagttttgttcgggttttgtatagtgataggagtat 2310
Qy 2230 CTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAA 2289
Db 2311 ttatattttggacgatttttttagtgttttagatgtttatgtgggtaattatatttttaa 2370
Qy 2290 TAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAGTTACA 2349
Db 2371 tagtgttattcggaaatattttaagtttaagatagttttgtttgttatttattagttata 2430
Qy 2350 GTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAAAGAGG 2409
Db 2431 gtatttggttgattgtgatgaagtgatttttatgaaagagggttgtattacggaaagagg 2490
Qy 2410 CACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAACCTGTT 2469

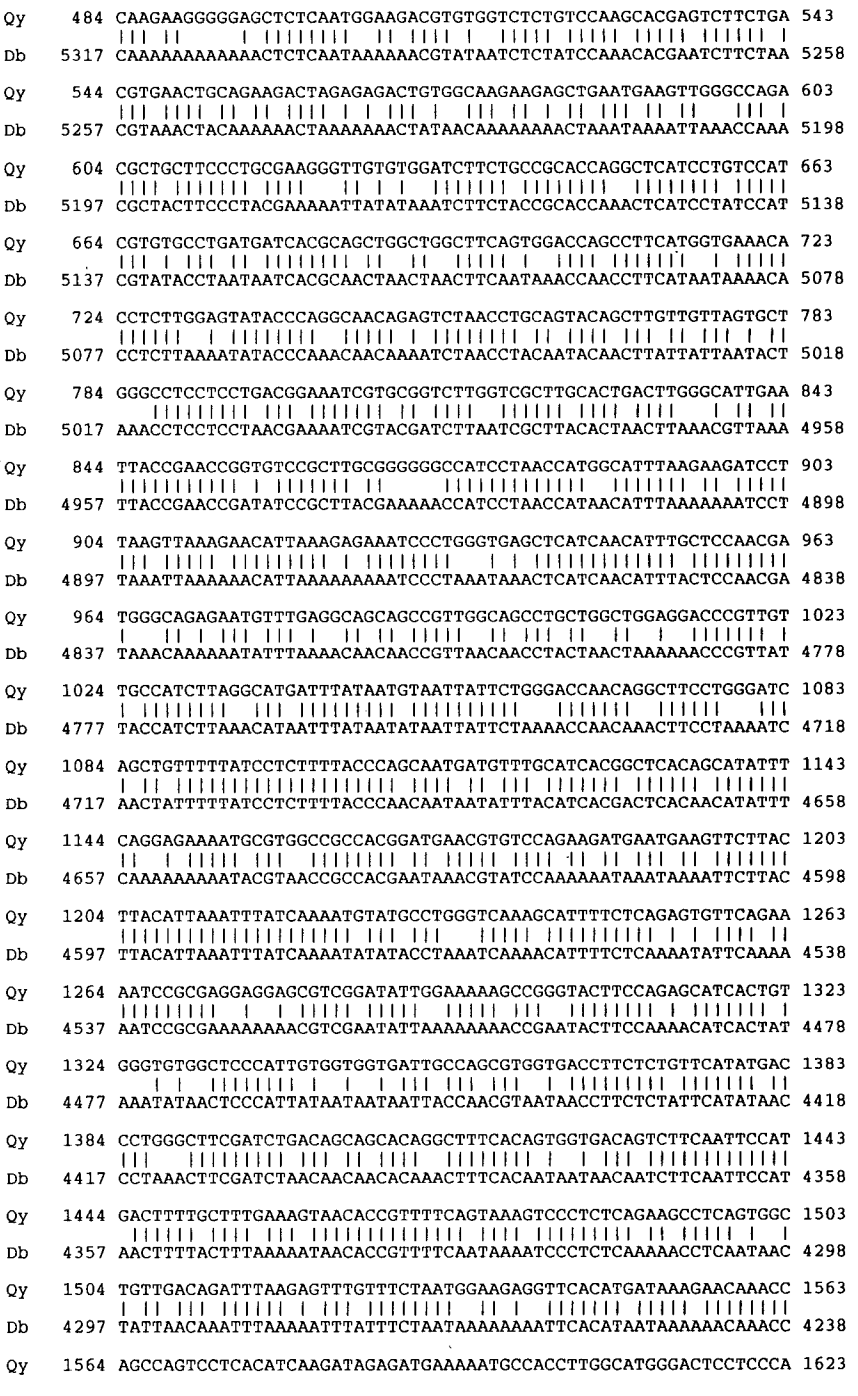

Db 2491 tatttatgaggaattgatgaatttaaatggtgattatgttattatttttaataatttgtt 2550
Qy 2470 GCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTCACAGAA 2529
Db 2551 gttgggagagatatcgttagttgagattaatttaaaaaaggaaattagtggtttatagaa 2610
Qy 2530 GAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGTAAAGCC 2589
Db 2611 gaagttataagataagggttttaaaatagattagtaaagaaggaaaaagtagtaaagtt 2670
Qy 2590 AGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGT 2649
Db 2671 agaggaagggtagtttgtgtagttggaagagaaagggtagggtttagtgttttggttagt 2730
Qy 2650 ATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGCCCT 2709
Db 2731 atatggtgtttatatttaggttgttgggggtttttggtattttggttattatggtttt 2790
Qy 2710 TTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAA 2769
Db 2791 ttttatgttgaatgtaggtagtatcgtttttagtatttggtggttgagttattggattaa 2850
Qy 2770 GCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGACAGCAT 2829
Db 2851 gtaaggaagcgggaatattattgtgattcgagggaacgagatttcggtgagtgatagtat 2910
Qy 2830 GAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCAT 2889
Db 2911 gaaggataatttttatatgtagtattatgttagtatttacgtttttttttatggtagttat 2970
Qy 2890 GCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTC 2949
Db 2971 gttgattttgaaagttattcgaggagttgtttttgttaagggtacgttgcgagtttttt 3030
Qy 2950 CCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACAC 3009
Db 3031 tcggttgtatgacgagtttttcgaaggatttttcgaagttttatgaagttttttgatac 3090
Qy 3010 GACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCG 3069
Db 3091 gattttatagggaggatttttaataggtttttaaagatatggatgaagttgacgtgcg 3150
Qy 3070 GCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGG 3129
Db 3151 gttgtcgttttaggtcgagatgtttatttagaacgttattttggtgtttttttgtgtggg 3210
Qy 3130 AATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTT 3189
Db 3211 aatgatcgtaggagtttttcgtggttttttgtggtagtggggttttttgttatttttt 3270
Qy 3190 TTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATAT 3249
Db 3271 tttagttttgtatattgtttttagggttttgattcgggagttgaagcgtttggataatat 3330
Qy 3250 CACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCA 3309
Db 3331 tacgtagttatttttttttttttatattacgtttagtatatagggttttgttattattta 3390
Qy 3310 CGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCA 3369
Db 3391 cgtttataataaagggtaggagtttttgtatagatattaggagttgttggatgataatta 3450
Qy 3370 AGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCAT 3429
Db 3451 agttttttttttttgtttacgtgtgcgatgcggtggttggttgtgcggttggatttat 3510
Qy 3430 CAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCC 3489
Db 3511 tagtatcgtttttattattattacggggttgatgatcgtttttatgtacgggtagatttt 3570
Qy 3490 CCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTT 3549
Db 3571 tttagtttatgcgggtttcgttatttttatgttgtttagttaacggggttgttttagtt 3630
Qy 3550 TACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCA 3609
Db 3631 tacggttagattggtatttgagatagaagttcgatttatttcggtggagaggattaatta 3690
Qy 3610 CTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCC 3669
Db 3691 ttatattaagattttgtttttggaagtatttgttagaattaagaataaggttttttttt 3750
Qy 3670 TGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAA 3729
Db 3751 tgattggttttaggagggagaggtgatttttgagaacgtagagatgaggtatcgagaaaa 3810
Qy 3730 CCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCAT 3789
Db 3811 ttttttttcgttttaaagaaagtatttttacgattaaatttaaagagaagattggtat 3870
Qy 3790 TGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGA 3849
Db 3871 tgtggggcggataggattagggaagttttcgttggggatggtttttttcgtttggtgga 3930
Qy 3850 GTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGA 3909
Db 3931 gttatttggaggttgtattaagattgatggagtgagaattagtgatattggttttgtcga 3990
Qy 3910 CCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAG 3969
Db 3991 ttttcgaagtaaatttttattattttttaagagtcggtgttgtttagtggtattgttag 4050
Qy 3970 ATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAG 4029
Db 4051 attaaatttggatttttttaattagtatattgaagattagatttgggatgttttggagag 4110
Qy 4030 GACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGA 4089
Db 4111 gatatatatgaaagaatgtattgtttagttatttttgaaatttgaatttgaagtgatgga 4170
Qy 4090 GAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCT 4149
Db 4171 gaatggggataatttttttagtgggggaacggtagtttttgtgtatagttagagttttgtt 4230
Qy 4150 CCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGA 4209
Db 4231 tcgttattgtaagatttgatttagatgaagttatagttgttatggatatagagataga 4290
Qy 4210 CTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGC 4269
Db 4291 tttattgatttaagagattattcgagaagtatttgtagattgtattatgttgattattgt 4350
Qy 4270 CCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGT 4329
Db 4351 ttatcgtttgtatacggttttaggtttcgataggattatggtgttggtttagggataggt 4410
Qy 4330 GGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGCCAT 4389
Db 4411 ggtggagtttgatattttatcggttttttgtttaacgatagttttcgattttatgttat 4470
Qy 4390 GTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGAAGT 4449
Db 4471 gtttgttgttgtagagaataaggtcgttgttaagggttgatttttttttgttgacgaagt 4530
Qy 4450 CTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCCTCC 4509
Db 4531 ttttttttttagagtattgttatttttgtttggggcggg-ttttttatcgcgtttttt 4589
Qy 4510 TACCGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTTGTG 4569
Db 4590 tatcgaaatttgtttttttcgattttatttttcgtatagtagtttcggattggtttgtg 4649
Qy 4570 TGTTTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGTAAA 4629
Db 4650 tgttttatttttagggagagttatattttgattattgtatttatttttatatttatgtaaa 4709

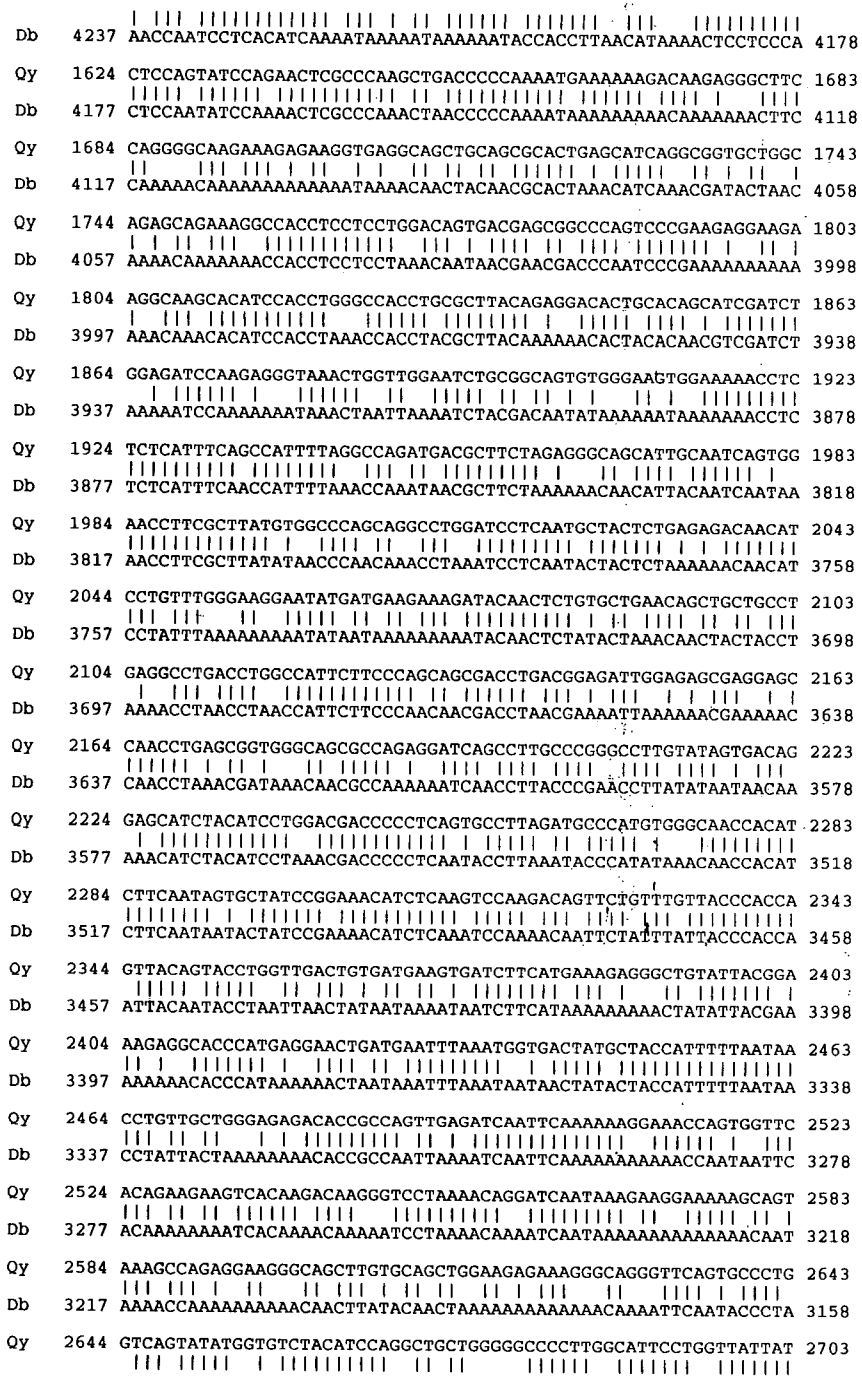


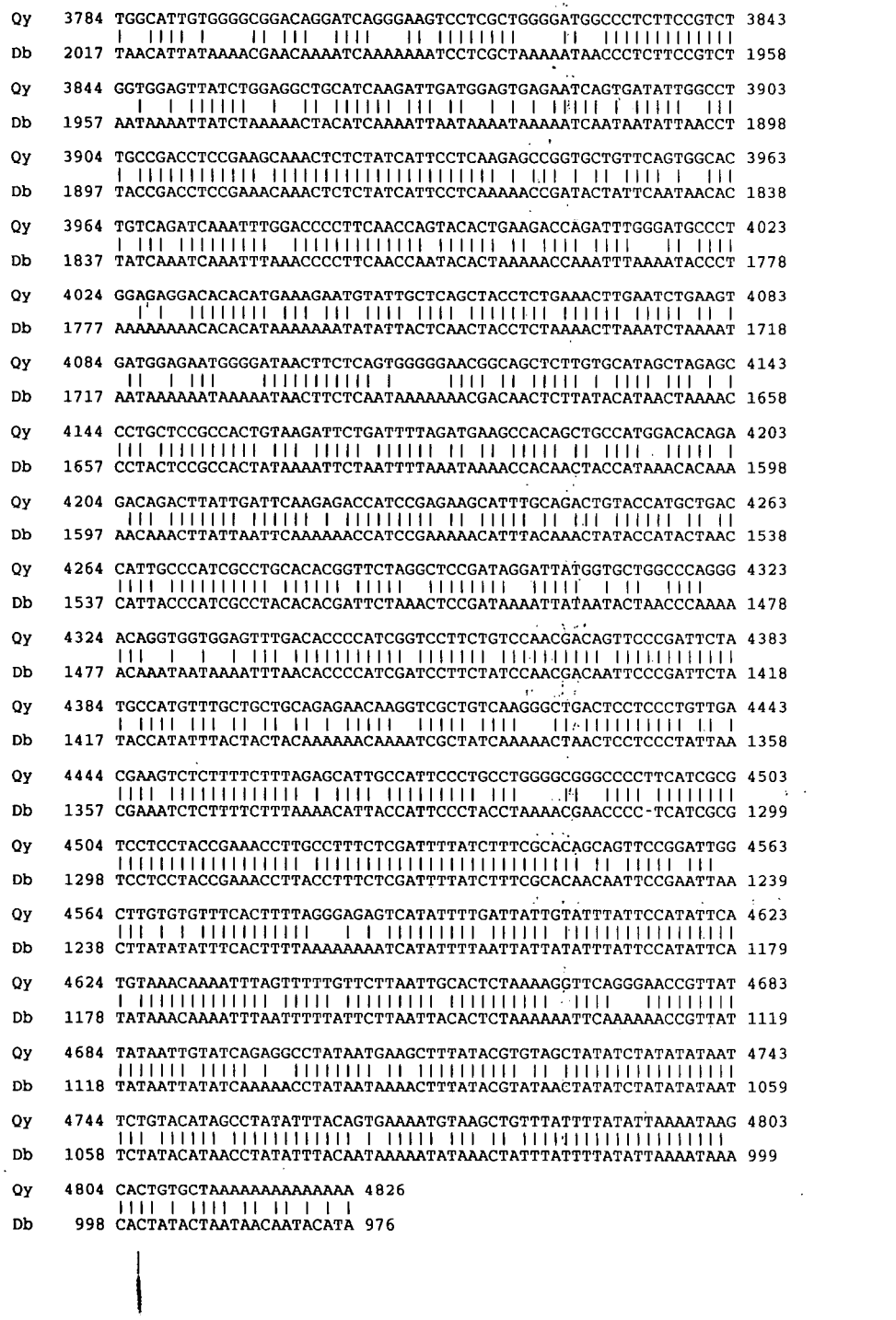
RESULT 6
US-10-172-086-82/c
; Sequence 82, Application US/10172086
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method and nucleic acids for the differentiation
; TITLE OF INVENTION: of prostate tumors
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/172,086
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 82
; LENGTH: 5881
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-82

Query Match 62.1%; Score 3011; DB 7; Length 5881;
Best Local Similarity 76.7%; Pred. No. 0;
Matches 3697; Conservative 0; Mismatches 1125; Indels 1; Gaps 1;

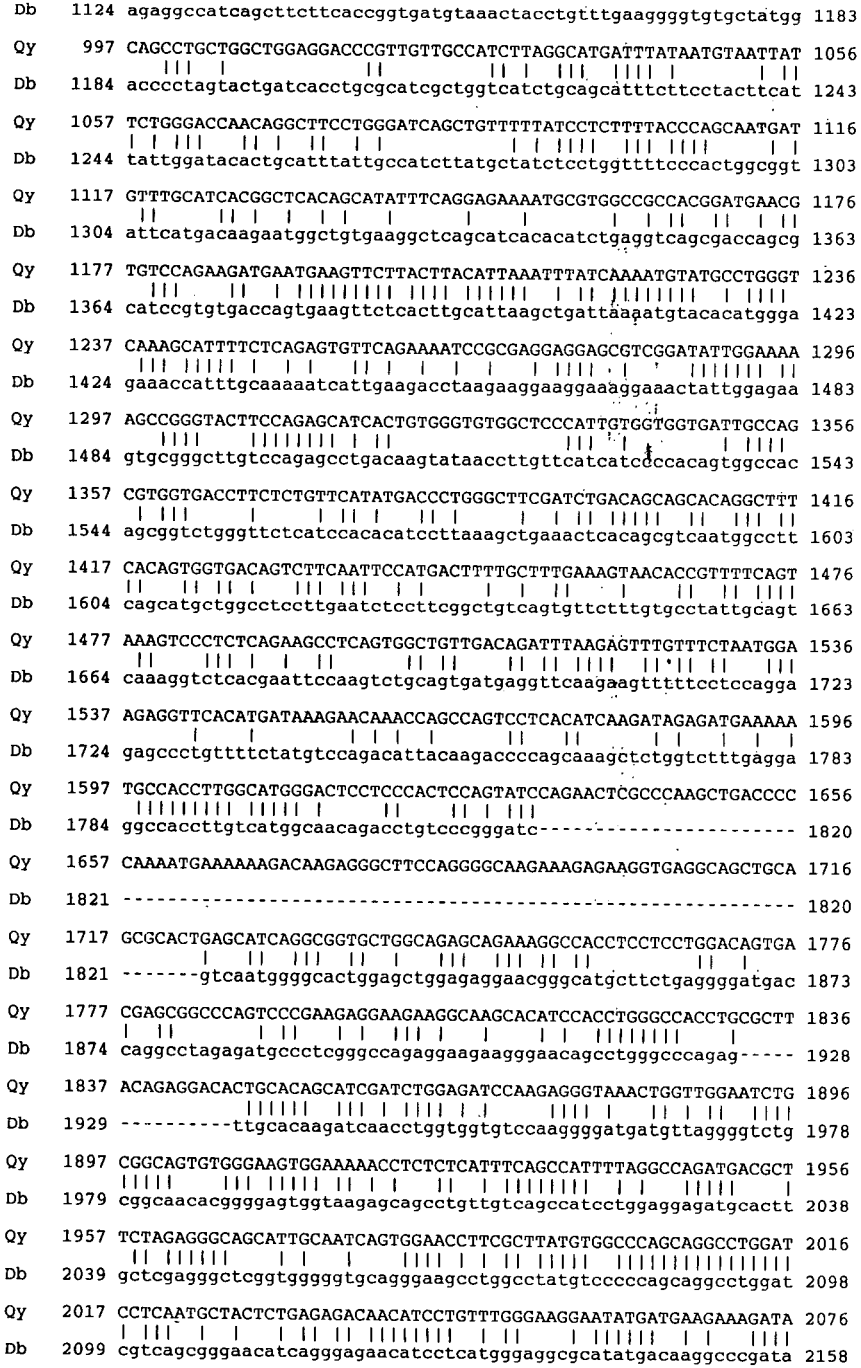





Db 4237 AACCAATCCTCACATCAAAATAAAAATAAAAAATACCACCTTAACATAAAACTCCTCCCA 4178
Qy 1624 CTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAGAGGGCTTC 1683
Db 4177 CTCCAATATCCAAAACTCGCCCAAACTAACCCCCAAAATAAAAAAAAACAAAAAAACTTC 4118
Qy 1684 CAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCGGTGCTGGC 1743
Db 4117 CAAAAACAAAAAAAAAAAAATAAAACAACTACAACGCACTAAACATCAAACGATACTAAC 4058
Qy 1744 AGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAAGAGGAAGA 1803
Db 4057 AAAACAAAAAAACCACCTCCTCCTAAACAATAACGAACGACCCAATCCCGAAAAAAAAAA 3998
Qy 1804 AGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCT 1863
Db 3997 AAACAAACACATCCACCTAAACCACCTACGCTTACAAAAAACACTACACAACGTCGATCT 3938
Qy 1864 GGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTC 1923
Db 3937 AAAAATCCAAAAAAATAAACTAATTAAAATCTACGACAATATAAAAAATAAAAAAACCTC 3878
Qy 1924 TCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGG 1983
Db 3877 TCTCATTTCAACCATTTTAAACCAAATAACGCTTCTAAAAAACAACATTACAATCAATAA 3818
Qy 1984 AACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACAT 2043
Db 3817 AACCTTCGCTTATATAACCCAACAAACCTAAATCCTCAATACTACTCTAAAAAACAACAT 3758
Qy 2044 CCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCT 2103
Db 3757 CCTATTTAAAAAAAAATATAATAAAAAAAAATACAACTCTATACTAAACAACTACTACCT 3698
Qy 2104 GAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGC 2163
Db 3697 AAAACCTAACCTAACCATTCTTCCCAACAACGACCTAACGAAAATTAAAAAACGAAAAAC 3638
Qy 2164 CAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAG 2223
Db 3637 CAACCTAAACGATAAACAACGCCAAAAAATCAACCTTACCCGAACCTTATATAATAACAA 3578
Qy 2224 GAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACAT 2283
Db 3577 AAACATCTACATCCTAAACGACCCCCTCAATACCTTAAATACCCATATAAACAACCACAT 3518
Qy 2284 CTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCA 2343
Db 3517 CTTCAATAATACTATCCGAAAACATCTCAAATCCAAAACAATTCTATTTATTACCCACCA 3458
Qy 2344 GTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGA 2403
Db 3457 ATTACAATACCTAATTAACTATAATAAAATAATCTTCATAAAAAAAAACTATATTACGAA 3398
Qy 2404 AAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAA 2463
Db 3397 AAAAAACACCCATAAAAAACTAATAAATTTAAATAATAACTATACTACCATTTTTAATAA 3338
Qy 2464 CCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACCAGTGGTTC 2523
Db 3337 CCTATTACTAAAAAAAACACCGCCAATTAAAATCAATTCAAAAAAAAAACCAATAATTC 3278
Qy 2524 ACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAAAGAAGGAAAAAGCAGT 2583
Db 3277 ACAAAAAAAATCACAAAACAAAAATCCTAAAACAAAATCAATAAAAAAAAAAAAAACAAT 3218
Qy 2584 AAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCAGTGCCCTG 2643
Db 3217 AAAACCAAAAAAAAAAACAACTTATACAACTAAAAAAAAAAAAAACAAAATTCAATACCCTA 3158
Qy 2644 GTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTAT 2703
Db 3157 ATCAATATATAATATCTACATCCAAACTACTAAAAACCCCTTAACATTCCTAATTATTAT 3098
Qy 2704 GGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTG 2763
Db 3097 AACCCTTTTCATACTAAATATAAACAACACCGCCTTCAACACCTAATAATTAAATTACTA 3038
Qy 2764 GATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTGA 2823
Db 3037 AATCAAACAAAAAAACGAAAACACCACTATAACTCGAAAAAACGAAACCTCGATAAATAA 2978
Qy 2824 CAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGC 2883
Db 2977 CAACATAAAAAACAATCCTCATATACAATACTATACCAACATCTACGCCCTCTCCATAAC 2918
Qy 2884 AGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGAGC 2943
Db 2917 AATCATACTAATCCTAAAAACCATTCGAAAAATTATCTTTATCAAAAACACGCTACGAAC 2858
Qy 2944 TTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTT 3003
Db 2857 TTCCTCCCGACTACATAACGAACTTTTCCGAAAAATCCTTCGAAACCCTATAAAATTTTT 2798
Qy 3004 TGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGA 3063
Db 2797 TAACACGACCCCCACAAAAAAAATTCTCAACAAATTTTCCAAAAACATAAATAAAATTAA 2738
Qy 3064 CGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTG 3123
Db 2737 CGTACGACTACCGTTCCAAACCGAAATATTCATCCAAAACGTTATCCTAATATTCTTCTA 2678
Qy 3124 TGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCAT 3183
Db 2677 TATAAAAATAATCGCAAAAATCTTCCCGTAATTCCTTATAACAATAAAACCCCTTATCAT 2618
Qy 3184 CCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGA 3243
Db 2617 CCTCTTTTCAATCCTACACATTATCTCCAAAATCCTAATTCGAAAACTAAAACGTCTAAA 2558
Qy 3244 CAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCAC 3303
Db 2557 CAATATCACGCAATCACCTTTCCTCTCCCACATCACGTCCAACATACAAAACCTTACCAC 2498
Qy 3304 CATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGA 3363
Db 2497 CATCCACGCCTACAATAAAAAACAAAAATTTCTACACAAATACCAAAAACTACTAAATAA 2438
Qy 3364 CAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGA 3423
Db 2437 CAACCAAACTCCTTTTTTTTTATTTACGTATACGATACGATAACTAACTATACGACTAAA 2378
Qy 3424 CCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCA 3483
Db 2377 CCTCATCAACATCGCCCTCATCACCACCACGAAACTAATAATCGTTCTTATACACGAACA 2318
Qy 3484 GATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTT 3543
Db 2317 AATTCCCCCAACCTATACGAATCTCGCCATCTCTTATACTATCCAATTAACGAAACTATT 2258
Qy 3544 CCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGAT 3603
Db 2257 CCAATTTACGATCAAACTAACATCTAAAACAAAAACTCGATTCACCTCGATAAAAAAAAT 2198
Qy 3604 CAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCC 3663
Db 2197 CAATCACTACATTAAAACTCTATCCTTAAAAACACCTACCAAAATTAAAAACAAAACTCC 2138
Qy 3664 CTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCG 3723
Db 2137 CTCCCCTAACTAACCCCAAAAAAAAAAAATAACCTTTAAAAACGCAAAAATAAAATACCG 2078
Qy 3724 AGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGAT 3783
Db 2077 AAAAAACCTCCCTCTCGTCCTAAAAAAAATATCCTTCACGATCAAACCTAAAAAAAAAAT 2018



```
RESULT   7
US-10-087-782A-1
; Sequence 1, Application US/10087782A
; GENERAL INFORMATION:
;  APPLICANT: AVENTIS PHARMA SA
;  APPLICANT:  US GOVERNMENT of the UNITED STATES
;  TITLE OF INVENTION: NUCLEIC ACID OF THE HUMAN ABCC11 GENE, VECTORS
;  TITLE OF INVENTION:  CONTAINING SUCH NUCLEIC ACID, AND USES THEREOF
;  FILE REFERENCE: ABCC11 GENE
;  CURRENT APPLICATION NUMBER: US/10/087,782A
;  CURRENT FILING DATE:  2002-07-03
;  PRIOR APPLICATION NUMBER: 60/272,757
;  PRIOR FILING DATE: 2001-03-05
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4862
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-087-782A-1


  Query Match             15.8%;  Score 768;  DB 6;  Length 4862;
  Best Local Similarity   50.9%;  Pred. No. 7.6e-138;
  Matches 2103;  Conservative    0;  Mismatches 1900;  Indels  125;  Gaps    7;
```


Db 1124 agaggccatcagcttcttcaccggtgatgtaaactacctgtttgaaggggtgtgctatgg 1183
Qy 997 CAGCCTGCTGGCTGGAGGACCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTAT 1056
Db 1184 acccctagtactgatcacctgcgcatcgctggtcatctgcagcatttcttcctacttcat 1243
Qy 1057 TCTGGGACCAACAGGCTTCCTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGAT 1116
Db 1244 tattggatacactgcatttattgccatcttatgctatctcctggttttcccactggcggt 1303
Qy 1117 GTTTGCATCACGGCTCACAGCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACG 1176
Db 1304 attcatgacaagaatggctgtgaaggctcagcatcacacatctgaggtcagcgaccagcg 1363
Qy 1177 TGTCCAGAAGATGAATGAAGTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGT 1236
Db 1364 catccgtgtgaccagtgaagttctcacttgcattaagctgattaaaatgtacacatggga 1423
Qy 1237 CAAAGCATTTTCTCAGAGTGTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAA 1296
Db 1424 gaaaccatttgcaaaaatcattgaagacctaagaaggaaggaaaggaaactattggagaa 1483
Qy 1297 AGCCGGGTACTTCCAGAGCATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAG 1356
Db 1484 gtgcgggcttgtccagagcctgacaagtataaccttgttcatcatcccacagtggccac 1543
Qy 1357 CGTGGTGACCTTCTCTGTTCATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTT 1416
Db 1544 agcggtctgggttctcatccacacatccttaaagctgaaactcacagcgtcaatggcctt 1603
Qy 1417 CACAGTGGTGACAGTCTTCAATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGT 1476
Db 1604 cagcatgctggcctccttgaatctccttcggctgtcagtgttctttgtgcctattgcagt 1663
Qy 1477 AAAGTCCCTCTCAGAAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGA 1536
Db 1664 caaaggtctcacgaattccaagtctgcagtgatgaggttcaagaagtttttcctccagga 1723
Qy 1537 AGAGGTTCACATGATAAAGAACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAA 1596
Db 1724 gagccctgttttctatgtccagacattacaagaccccagcaaagctctggtctttgagga 1783
Qy 1597 TGCCACCTTGGCATGGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCC 1656
Db 1784 ggccaccttgtcatggcaacagacctgtcccgggatc---------- 1820
Qy 1657 CAAAATGAAAAAAGACAAGAGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCA 1716
Db 1821 ---------- 1820
Qy 1717 GCGCACTGAGCATCAGGCGGTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGA 1776
Db 1821 -------gtcaatggggcactggagctggagaggaacgggcatgcttctgaggggatgac 1873
Qy 1777 CGAGCGGCCCAGTCCCGAAGAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTT 1836
Db 1874 caggcctagagatgccctcgggccagaggaagaagggaacagcctgggcccagag----- 1928
Qy 1837 ACAGAGGACACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTG 1896
Db 1929 ----------ttgcacaagatcaacctggtggtgtccaaggggatgatgttaggggtctg 1978
Qy 1897 CGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCT 1956
Db 1979 cggcaacacggggagtggtaagagcagcctgttgtcagccatcctggaggagatgcactt 2038
Qy 1957 TCTAGAGGGCAGCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGAT 2016
Db 2039 gctcgagggctcggtgggggtgcagggaagcctggcctatgtccccagcaggcctggat 2098
Qy 2017 CCTCAATGCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATA 2076
Db 2099 cgtcagcgggaacatcagggagaacatcctcatgggaggcgcatatgacaaggcccgata 2158
Qy 2077 CAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGA 2136
Db 2159 cctccaggtgctccactgctgctccctgaatcgggacctggaacttctgccctttggaga 2218
Qy 2137 CCTGACGGAGATTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAG 2196
Db 2219 catgacagagattggagagcggggcctcaacctctctgggggggcagaaacagaggatcag 2278
Qy 2197 CCTTGCCCGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGC 2256
Db 2279 cctggcccgcgccgtctattccgaccgtcagatctacctgctggacgacccccctgtctgc 2338
Qy 2257 CTTAGATGCCCATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTC 2316
Db 2339 tgtggacgcccacgtggggaagcacatttttgaggagtgcattaagaagacactcagggg 2398
Qy 2317 CAAGACAGTTCTGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGAT 2376
Db 2399 gaagacggtcgtcctggtgacccaccagctgcagtacttagaattttgtggccagatcat 2458
Qy 2377 CTTCATGAAAGAGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAA 2436
Db 2459 tttgttggaaaatgggaaaatctgtgaaaatggaactcacagtgagttaatgcagaaaaa 2518
Qy 2437 TGGTGACTATGCTACCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGAT 2496
Db 2519 ggggaaatatgcccaacttatccagaagatgcacaaggaagccacttcggacatgttgca 2578
Qy 2497 CAATTCAAAAAAGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAAC 2556
Db 2579 ggacacagcaaagatagcagagaagccaaaggtagaaagtcaggctctggccacctccct 2638
Qy 2557 AGGATCAATAAAGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGA 2616
Db 2639 ggaagagtctctcaacggaaatgctgt------gccggagcatcagctcacacaggagga 2692
Qy 2617 AGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGG 2676
Db 2693 ggagatggaagaaggctccttgagttggagggtctaccaccactacatccaggcagctgg 2752
Qy 2677 GGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGC 2736
Db 2753 aggttacatggtctcttgcataatttttcttcttcgtggtgctgatcgtcttcttaacgat 2812
Qy 2737 CTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGAC 2796
Db 2813 cttcagcttctggtggctgagctactggttggagcagggctcggggaccaatagcagccg 2872
Qy 2797 TCGAGGGAACGAGACC---TCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTA 2853
Db 2873 agagagcaatggaaccatggcagacctgggcaacattgcagacaatcctcaactgtcctt 2932
Qy 2854 CTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGG 2913
Db 2933 ctaccagctggtgtacgggctcaacgccctgctcctcatctgtgtgggggtctgctcctc 2992
Qy 2914 AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCG 2973
Db 2993 agggattttcaccaaagtcacgaggaaggcatccacggccctgcacaacaagctcttcaa 3052
Qy 2974 AAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAA 3033
Db 3053 caaggttttccgctgccccatgagtttctttgacaccatcccaataggccggcttttgaa 3112
Qy 3034 CAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTT 3093
Db 3113 ctgcttcgcaggggacttggaacagctggaccagctcttgcccatcttttcagagcagtt 3172
Qy 3094 CATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTG 3153
Db 3173 cctggtcctgtccttaatggtgatcgccgtcctgttgattgtcagtgtgctgtctccata 3232

```
Qy   3154 GTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAG 3213
Db   3233 tatcctgttaatgggagccataatcatggttatttgcttcatttattatatgatgttcaa 3292

Qy   3214 GGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCA 3273
Db   3293 gaaggccatcggtgtgttcaagagactggagaactatagccggtctcctttattctccca 3352

Qy   3274 CATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTT 3333
Db   3353 catcctcaattctctgcaaggcctgagctccatccatgtctatggaaaaactgaagactt 3412

Qy   3334 TCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTG 3393
Db   3413 catcagccagtttaagaggctgactgatgcgcagaataactacctgctgttgtttctatc 3472

Qy   3394 TGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCAC 3453
Db   3473 ttccacacgatggatggcattgaggctggagatcatgaccaaccttgtgaccttggctgt 3532

Qy   3454 GGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCAT 3513
Db   3533 tgccctgttcgtggcttttggcatttcctccacccccctactcctttaaagtcatggctgt 3592

Qy   3514 CTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGAC 3573
Db   3593 caacatcgtgctgcagctggcgtccagcttccaggccactgcccggattggcttggagac 3652

Qy   3574 AGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGA 3633
Db   3653 agaggcacagttcacggctgtagagaggatactgcagtacatgaagatgtgtgtctcgga 3712

Qy   3634 AGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGT 3693
Db   3713 agctcctttacacatggaaggcacaagttgtccccaggggtggccacagcatggggaaat 3772

Qy   3694 GACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGT 3753
Db   3773 catatttcaggattatcacatgaaatacagagacaacacacccaccgtgcttcacggcat 3832

Qy   3754 ATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAA 3813
Db   3833 caacctgaccatccgcggccacgaagtggtgggcatcgtgggaaggacgggctctgggaa 3892

Qy   3814 GTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGAT 3873
Db   3893 gtcctccttgggcatggctctcttccgcctggtggagcccatggcaggccggattctcat 3952

Qy   3874 TGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCAT 3933
Db   3953 tgacggcgtggacatttgcagcatcggcctggaggacttgcggtccaagctctcagtgat 4012

Qy   3934 TCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCA 3993
Db   4013 ccctcaagatccagtgctgctctcaggaaccatcagattcaacctagatccctttgaccg 4072

Qy   3994 GTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGC 4053
Db   4073 tcacactgaccagcagatctgggatgccttggagaggacattcctgaccaaggccatctc 4132

Qy   4054 TCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGG 4113
Db   4133 aaagttccccaaaaagctgcatacagatgtggtggaaaacggtggaaacttctctgtggg 4192

Qy   4114 GGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTT 4173
Db   4193 ggagaggcagctgctctgcattgccagggctgtgcttcgcaactccaagatcatccttat 4252

Qy   4174 AGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCG 4233
Db   4253 cgatgaagccacagcctccattgacatggagacagacaccctgatccagcgcacaatccg 4312

Qy   4234 AGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGG 4293

Db   4313 tgaagccttccagggctgcaccgtgctcgtcattgcccaccgtgtcaccactgtgctgaa 4372

Qy   4294 CTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGT 4353
Db   4373 ctgtgaccacatcctggttatgggcaatgggaaggtggtagaatttgatcggccggaggt 4432

Qy   4354 CCTTCTGTCCAACGACAGTTCCCGATTCTATGCCATGTTTGCTGCTGC 4401
Db   4433 actgcggaagaagcctgggtcattgttcgcagccctcatggccacagc 4480
```

RESULT 8
US-10-162-012-35
; Sequence 35, Application US/10162012
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 4083
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-012-35

Query Match 15.0%; Score 725.4; DB 7; Length 4083;

```
Best Local Similarity   55.8%;  Pred. No. 1.1e-129;
Matches 1427;  Conservative    0;  Mismatches 1121;  Indels    9;  Gaps    2;

Qy   1848 TGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGG 1907
Db   1514 tgcacaagatcaacctggtggtgtccaaggggatgatgttaggggtctgcggcaacacgg 1573

Qy   1908 GAAGTGGAAAAACCTCTCTCATTTCAGCCATTTAGGCCAGATGACGCTTCTAGAGGGCA 1967
Db   1574 ggagtggtaagagcagcctgttgtcagccatcctggaggagatgcacttgctcgagggct 1633

Qy   1968 GCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTA 2027
Db   1634 cggtgggggtgcagggaagcctggcctatgtcccccagcaggcctggatcgtcagcggga 1693

Qy   2028 CTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGC 2087
Db   1694 acatcagggagaacatcctcatgggaggcgcatatgacaaggcccgatacctccaggtgc 1753

Qy   2088 TGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGA 2147
Db   1754 tccactgctgctccctgaatcgggacctggaacttctgccctttggagacatgacagaga 1813

Qy   2148 TTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGG 2207
Db   1814 ttggagagcggggcctcaacctctctggggggcagaaacagaggatcagcctggcccgcg 1873

Qy   2208 CCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCC 2267
Db   1874 ccgtctattccgaccgtcagatctacctgctggacgacccccctgtctgctgtggacgccc 1933

Qy   2268 ATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTC 2327
Db   1934 acgtggggaagcacatttttgaggagtgcattaagaagacactcaggggggaagacggtcg 1993

Qy   2328 TGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAG 2387
Db   1994 tcctggtgacccaccagctgcagtacttagaattttgtggccagatcattttgttggaaa 2053

Qy   2388 AGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATG 2447
Db   2054 atgggaaaatctgtgaaaatggaactcacagtgagttaatgcagaaaaaggggaaatatg 2113

Qy   2448 CTACCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAA 2507
Db   2114 cccaacttatccagaagatgcacaaggaagccacttcggacatgttgcaggacacagcaa 2173

Qy   2508 AGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAA 2567
Db   2174 agatagcagagaagccaaaggtagaaagtcaggctctggccacctccctggaagagtctc 2233

Qy   2568 AGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGC 2627
Db   2234 tcaacggaaatgctgtgc------cggagcatcagctcacacaggaggaggagatggaag 2287

Qy   2628 AGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGG 2687
Db   2288 aaggctccttgagttggagggtctaccaccactacatccaggcagctggaggttacatgg 2347

Qy   2688 CATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCT 2747
Db   2348 tctcttgcataatttcttctttgtggtgctgatcgtcttcttaacgatcttcagcttct 2407

Qy   2748 GGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACG 2807
Db   2408 ggtggctgagctactggttggagcagggctcggggaccaatagcagccgagagagcaatg 2467

Qy   2808 AGACCTCGGTGA---GTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCA 2864
Db   2468 gaaccatggcagacctgggcaacattgcagacaatcctcaactgtccttctaccagctgg 2527

Qy   2865 TCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTG 2924
Db   2528 tgtacgggctcaacgccctgctcctcatctgtgtgggggtctgctcctcagggattttca 2587

Qy   2925 TCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTC 2984
Db   2588 ccaaagtcacgaggaaggcatccacggccctgcacaacaagctcttcaacaaggtttcc 2647

Qy   2985 GAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCA 3044
Db   2648 gctgccccatgagtttctttgacaccatcccaataggccggcttttgaactgcttcgcag 2707

Qy   3045 AAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACG 3104
Db   2708 gggacttggaacagctggaccagctcttgcccatcttttcagagcagttcctggtcctgt 2767

Qy   3105 TTATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGG 3164
Db   2768 ccttaatggtgatcgccgtcctgttgattgtcagtgtgctgtctccatatatcctgttaa 2827

Qy   3165 CAGTGGGGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTC 3224
Db   2828 tgggagccataatcatggttatttgcttcatttattatatgatgttcaagaaggccatcg 2887

Qy   3225 GGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCA 3284
Db   2888 gtgtgttcaagagactggagaactatagccggtctccttattctcccacatcctcaatt 2947

Qy   3285 GCATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGAT 3344
Db   2948 ctctgcaaggcctgagctccatccatgtctatggaaaaactgaagacttcatcagccagt 3007

Qy   3345 ACCAGGAGCTGCTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGT 3404
Db   3008 ttaagaggctgactgatgcgcagaataactacctgctgttgtttctatcttccacacgat 3067

Qy   3405 GGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGA 3464
Db   3068 ggatggcattgaggctggagatcatgaccaaccttgtgaccttggctgttgccctgttcg 3127

Qy   3465 TCGTTCTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTG 3524
Db   3128 tggcttttggcatttcctccacccccctactcctttaaagtcatggctgtcaacatcgtgc 3187

Qy   3525 TCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGAT 3584
Db   3188 tgcagctggcgtccagcttccaggccactgcccggattggcttggagacagaggcacagt 3247

Qy   3585 TCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCA 3644
Db   3248 tcacggctgtagagaggatactgcagtacatgaagatgtgtgtctcggaagctcctttac 3307

Qy   3645 GAATTAAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGA 3704
Db   3308 acatggaaggcacaagttgtccccaggggtggccacagcatggggaaatcatatttcagg 3367

Qy   3705 ACGCAGAGATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGA 3764
Db   3368 attatcacatgaaatacagagacaacacacccaccgtgcttcacggcatcaacctgacca 3427

Qy   3765 TCAAACCTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGG 3824
Db   3428 tccgcggccacgaagtggtgggcatcgtgggaaggacgggctctgggaagtcctccttgg 3487

Qy   3825 GGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGA 3884
Db   3488 gcatggctctcttccgcctggtggagcccatggcaggccggattctcattgacggcgtgg 3547

Qy   3885 GAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGC 3944
Db   3548 acatttgcagcatcggcctggaggacttgcggtccaagctctcagtgatccctcaagatc 3607

Qy   3945 CGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAG 4004
Db   3608 cagtgctgctctcaggaaccatcagattcaacctagatcccttgaccgtcacactgacc 3667
```

```
Qy   4005 ACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTC 4064
          | ||||| |||||||||| ||||||||||  | |||   |    ||  |  || | ||
Db   3668 agcagatctgggatgccttggagaggacattcctgaccaaggccatctcaaagttcccca 3727

Qy   4065 TGAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGC 4124
            || ||  |  | || ||| |||| || || |  |||||||| |||||||| ||||||
Db   3728 aaaagctgcatacagatgtggtggaaaacggtggaaacttctctgtgggggagaggcagc 3787

Qy   4125 TCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCA 4184
          |  | ||||| || || ||  |||| ||| |||  |||||  |  || | ||||||||||
Db   3788 tgctctgcattgccagggctgtgcttcgcaactccaagatcatccttatcgatgaagcca 3847

Qy   4185 CAGCTGCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTG 4244
          ||||  |||| ||||  |||||||||    |||| ||    || |||| |||| ||
Db   3848 cagcctccattgacatggagacagacaccctgatccagcgcacaatccgtgaagccttcc 3907

Qy   4245 CAGACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGA 4304
            | ||| ||| ||||   |||||||||| ||  |   ||| || ||   ||  ||    |
Db   3908 agggctgcaccgtgctcgtcattgcccaccgtgtcaccactgtgctgaactgtgaccaca 3967

Qy   4305 TTATGGTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCA 4364
          |  ||||  ||| | | ||  ||||||| || |||||    ||   ||| || | |   |
Db   3968 tcctggttatgggcaatgggaaggtggtagaatttgatcggccggaggtactgcggaaga 4027

Qy   4365 ACGACAGTTCCCGATTCTATGCCATGTTTGCTGCTGC 4401
          |     | ||    |||   ||| |  | ||  | ||
Db   4028 agcctgggtcattgttcgcagccctcatggccacagc 4064


RESULT   9
US-10-162-012-33
; Sequence 33, Application US/10162012
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 4638
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)...(4280)
US-10-162-012-33


  Query Match             15.0%;  Score 725.4;  DB 7;  Length 4638;
  Best Local Similarity   55.8%;  Pred. No. 1.1e-129;
  Matches 1427;  Conservative    0;  Mismatches 1121;  Indels    9;  Gaps    2;

Qy   1848 TGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGG 1907
           ||||||  ||| | |||| | |     |||| |   || | ||  |||||||||    ||
Db   1714 tgcacaagatcaacctggtggtgtccaaggggatgatgttaggggtctgcggcaacacgg 1773

Qy   1908 GAAGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCA 1967
           | ||||| || | |   ||  | ||||||||  | |   |||||    | || ||||||
Db   1774 ggagtggtaagagcagcctgttgtcagccatcctggaggagatgcacttgctcgagggct 1833

Qy   1968 GCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTA 2027
              | |   |    |||| | | || |||||  |||||||||||||||||| |||  |  |
Db   1834 cggtgggggtgcagggaagcctggcctatgtcccccagcaggcctggatcgtcagcggga 1893

Qy   2028 CTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGC 2087
             | || || ||||||||  | ||    | ||||||  | |   |||||  |   ||||
Db   1894 acatcagggagaacatcctcatgggaggcgcatatgacaaggcccgatacctccaggtgc 1953

Qy   2088 TGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGA 2147
           |  || |||||| |||||  |  |||||||   |||| |||    | ||| |||| ||||
Db   1954 tccactgctgctccctgaatcgggacctggaacttctgccctttggagacatgacagaga 2013

Qy   2148 TTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGG 2207
           ||||||||||| ||   ||||||    || ||||||   |||||||||||||| ||||| |
Db   2014 ttggagagcggggcctcaacctctctgggggggcagaaacagaggatcagcctggcccgcg 2073

Qy   2208 CCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCC 2267
           || | |||   ||| |    |||||| | ||||||||||||||   |||  | || ||||
Db   2074 ccgtctattccgaccgtcagatctacctgctggacgacccccctgtctgctgtggacgccc 2133

Qy   2268 ATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTC 2327
           | ||||| || ||||| ||  |       ||   |||    |||| |   ||||| ||
Db   2134 acgtggggaagcacatttttgaggagtgcattaagaagacactcagggggaagacggtcg 2193

Qy   2328 TGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAG 2387
           |  | || |||||||||| | ||||||| | |      ||||   |  | || ||  || ||
Db   2194 tcctggtgacccaccagctgcagtacttagaattttgtggccagatcattttgttggaaa 2253

Qy   2388 AGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATG 2447
           | ||    ||    ||||  || || ||    ||  | ||| |   ||| ||  | ||||
Db   2254 atgggaaaatctgtgaaaatggaactcacagtgagttaatgcagaaaaaggggaaatatg 2313

Qy   2448 CTACCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAA 2507
           |     || |  | ||  ||     || ||  ||  ||    |   |    |  ||  ||
Db   2314 cccaacttatccagaagatgcacaaggaagccacttcggacatgttgcaggacacagcaa 2373

Qy   2508 AGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAATAA 2567
           ||  | |        || ||    |    || |    ||   |        | |
Db   2374 agatagcagagaagccaaaggtagaaagtcaggctctggccacctccctggaagagtctc 2433

Qy   2568 AGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGC 2627
```

```
Db   2434 tcaacggaaatgctgtgc------cggagcatcagctcacacaggaggaggagatggaag 2487

Qy   2628 AGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGG 2687
Db   2488 aaggctccttgagttggagggtctaccaccactacatccaggcagctggaggttacatgg 2547

Qy   2688 CATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCT 2747
Db   2548 tctcttgcataatttttcttctttgtggtgctgatcgtcttcttaacgatcttcagcttct 2607

Qy   2748 GGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACG 2807
Db   2608 ggtggctgagctactggttggagcagggctcggggaccaatagcagccgagagagcaatg 2667

Qy   2808 AGACCTCGGTGA---GTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCA 2864
Db   2668 gaaccatggcagacctgggcaacattgcagacaatcctcaactgtccttctaccagctgg 2727

Qy   2865 TCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTG 2924
Db   2728 tgtacgggctcaacgccctgctcctcatctgtgtgggggtctgctcctcagggattttca 2787

Qy   2925 TCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTC 2984
Db   2788 ccaaagtcacgaggaaggcatccacggccctgcacaacaagctcttcaacaaggttttcc 2847

Qy   2985 GAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCA 3044
Db   2848 gctgccccatgagtttctttgacaccatcccaataggccggcttttgaactgcttcgcag 2907

Qy   3045 AAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACG 3104
Db   2908 gggacttggaacagctggaccagctcttgcccatcttttcagagcagttcctggtcctgt 2967

Qy   3105 TTATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGG 3164
Db   2968 ccttaatggtgatcgccgtcctgttgattgtcagtgtgctgtctccatatatcctgttaa 3027

Qy   3165 CAGTGGGGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTC 3224
Db   3028 tgggagccataatcatggttatttgcttcatttattatatgatgttcaagaaggccatcg 3087

Qy   3225 GGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCA 3284
Db   3088 gtgtgttcaagagactggagaactatagccggtctccttattctcccacatcctcaatt 3147

Qy   3285 GCATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGAT 3344
Db   3148 ctctgcaaggcctgagctccatccatgtctatggaaaaactgaagacttcatcagccagt 3207

Qy   3345 ACCAGGAGCTGCTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGT 3404
Db   3208 ttaagaggctgactgatgcgcagaataactacctgctgttgtttctatcttccacacgat 3267

Qy   3405 GGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGA 3464
Db   3268 ggatggcattgaggctggagatcatgaccaaccttgtgaccttggctgttgccctgttcg 3327

Qy   3465 TCGTTCTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTG 3524
Db   3328 tggcttttggcatttcctccacccccctactcctttaaagtcatggctgtcaacatcgtgc 3387

Qy   3525 TCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGAT 3584
Db   3388 tgcagctggcgtccagcttccaggccactgcccggattggcttggagacagaggcacagt 3447

Qy   3585 TCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCA 3644
Db   3448 tcacggctgtagagaggatactgcagtacatgaagatgtgtgtctcggaagctcctttac 3507

Qy   3645 GAATTAAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGA 3704

Db   3508 acatggaaggcacaagttgtccccaggggtggccacagcatggggaaatcatatttcagg 3567

Qy   3705 ACGCAGAGATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGA 3764
Db   3568 attatcacatgaaatacagagacaacacacccaccgtgcttcacggcatcaacctgacca 3627

Qy   3765 TCAAACCTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGG 3824
Db   3628 tccgcggccacgaagtggtgggcatcgtgggaaggacgggctctgggaagtcctccttgg 3687

Qy   3825 GGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGA 3884
Db   3688 gcatggctctcttccgcctggtggagcccatggcaggccggattctcattgacggcgtgg 3747

Qy   3885 GAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGC 3944
Db   3748 acatttgcagcatcggcctggaggacttgcggtccaagctctcagtgatccctcaagatc 3807

Qy   3945 CGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAG 4004
Db   3808 cagtgctgctctcaggaaccatcagattcaacctagatccctttgaccgtcacactgacc 3867

Qy   4005 ACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTC 4064
Db   3868 agcagatctgggatgccttggagaggacattcctgaccaaggccatctcaaagttcccca 3927

Qy   4065 TGAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGC 4124
Db   3928 aaaagctgcatacagatgtggtggaaaacggtggaaacttctctgtgggggagaggcagc 3987

Qy   4125 TCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCA 4184
Db   3988 tgctctgcattgccagggctgtgcttcgcaactccaagatcatccttatcgatgaagcca 4047

Qy   4185 CAGCTGCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTG 4244
Db   4048 cagcctccattgacatggagacagacaccctgatccagcgcacaatccgtgaagccttcc 4107

Qy   4245 CAGACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGA 4304
Db   4108 agggctgcaccgtgctcgtcattgcccaccgtgtcaccactgtgctgaactgtgaccaca 4167

Qy   4305 TTATGGTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCA 4364
Db   4168 tcctggttatgggcaatgggaaggtggtagaatttgatcggccggaggtactgcggaaga 4227

Qy   4365 ACGACAGTTCCCGATTCTATGCCATGTTTGCTGCTGC 4401
Db   4228 agcctgggtcattgttcgcagccctcatggccacagc 4264
```

```
RESULT 10
US-10-137-337-228
; Sequence 228, Application US/10137337
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PM028C1N
;  CURRENT APPLICATION NUMBER: US/10/137,337
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: 09/758,447
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  NUMBER OF SEQ ID NOS: 812
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 228
;   LENGTH: 1579
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
```

```
;   NAME/KEY: misc_feature
;   LOCATION: (927)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-137-337-228


  Query Match             12.2%;  Score 591.8;  DB 7;  Length 1579;
  Best Local Similarity   99.5%;  Pred. No. 4.1e-104;
  Matches  604;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy   4213 ATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCA 4272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 attgattcaagagaccatccgagaagcatttgcagactgtaccatgctgaccattgccca 60

Qy   4273 TCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGT 4332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 tcgcctgcacacggttctaggctccgataggattatggtgctggcccagggacaggtggt 120

Qy   4333 GGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCCCGATTCTATGCCATGTT 4392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ggagtttgacaccccatcggtccttctgtccaacgacagttcccgattctatgccatgtt 180

Qy   4393 TGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTCCTCCCTGTTGACGAAGTCTC 4452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 tgctgctgcagagaacaaggtcgctgtcaagggctgactcctccctgttgacgaagtctc 240

Qy   4453 TTTTCTTTAGAGCATTGCCATTCCCTGCCTGGGGCGGGCCCCTTCATCGCGTCCTCCTAC 4512
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    241 ttttctttagagcattgccattccctgcctggggcgggcccc-tcatcgcgtcctcctac 299

Qy   4513 CGAAACCTTGCCTTTCTCGATTTTATCTTTCGCACAGCAGTTCCGGATTGGCTTGTGTGT 4572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 cgaaaccttgcctttctcgattttatctttcgcacagcagttccggattggcttgtgtgt 359

Qy   4573 TTCACTTTTAGGGAGAGTCATATTTTGATTATTGTATTTATTCCATATTCATGTAAACAA 4632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 ttcacttttagggagagtcatattttgattattgtatttattccatattcatgtaaacaa 419

Qy   4633 AATTTAGTTTTTGTTCTTAATTGCACTCTAAAAGGTTCAGGGAACCGTTATTATAATTGT 4692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 aatttagtttttgttcttaattgcactctaaaaggttcagggaaccgttattataattgt 479

Qy   4693 ATCAGAGGCCTATAATGAAGCTTTATACGTGTAGCTATATCTATATATAATTCTGTACAT 4752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 atcagaggcctataatgaagctttatacgtgtagctatatctatatataattctgtacat 539

Qy   4753 AGCCTATATTTACAGTGAAAATGTAAGCTGTTTATTTTATATTAAAATAAGCACTGTGCT 4812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 agcctatatttacagtgaaaatgtaagctgtttattttatattaaaataagcactgtgct 599

Qy   4813 AAAAAAA 4819
          || || |
Db    600 aataaca 606


RESULT  11
PCT-US02-07787-35
; Sequence 35, Application PC/TUS0207787
; GENERAL INFORMATION:
;  APPLICANT: The Brigham and Women's Hospital, Inc.
;  APPLICANT:  Yates, Karen
;  APPLICANT:  Mizuno, Shuichi
;  APPLICANT:  Glowacki, Julie
;  TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
;  FILE REFERENCE: B0801/7244/KA/ERP
;  CURRENT APPLICATION NUMBER: PCT/US02/07787
;  CURRENT FILING DATE:  2002-03-12
;  PRIOR APPLICATION NUMBER: US 60/274,980
;  PRIOR FILING DATE: 2001-03-12
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
;   LENGTH: 5011
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-07787-35


  Query Match             10.5%;  Score 511.2;  DB 1;  Length 5011;
  Best Local Similarity   52.5%;  Pred. No. 1.4e-88;
  Matches 1367;  Conservative    0;  Mismatches 1178;  Indels   59;  Gaps    9;

Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
          ||||| ||||||||||||   | ||   |      ||||||  |  |||||    |    |||
Db   2143 cacattcacctgggcca--ggagcgaccctcccacactgaatggcatcaccttctccatc 2200

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
          |  ||  |||    ||||  |   |    |||   |||||  | |||||  | ||  ||  |
Db   2201 cccgaaggtgctttggtggccgtggtgggccaggtgggctgcggaaagtcgtccctgctc 2260

Qy   1931 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCAATCAGTGGAACCTTC 1990
          ||||||  | ||  |   |||||       | |||||   |  |  ||  ||||  ||  || |
Db   2261 tcagccctcttggctgagatggacaaagtggaggggcacgtggctatcaagggctccgtg 2320

Qy   1991 GCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGAGACAACATCCTGTTT 2050
          ||  ||||||  |  ||||||||||||||  |   ||||  |  ||||   ||||  ||||||||  |||
Db   2321 gcctatgtgccacagcaggcctggattcagaatgattctctccgagaaaacatccttttt 2380

Qy   2051 GGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGCTGCTGCCTGAGGCCT 2110
          ||     |    ||  |||  |   ||||  ||  |||  |   |   |||   |||     ||
Db   2381 ggatgtcagctggaggaaccatattacaggtccgtgatacaggcctgtgccctcctccca 2440

Qy   2111 GACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAGCGAGGAGCCAACCTG 2170
          |||||||  ||  ||  |||||  |  ||  |  |||  ||||||||  |||    ||  |   ||||||
Db   2441 gacctggaaatcctgcccagtggggatcggacagagattggcgagaagggcgtgaacctg 2500

Qy   2171 AGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTATAGTGACAGGAGCATC 2230
             ||  ||  |||    |||  |   |  ||||  ||||||||  ||||     ||     |||
Db   2501 tctgggggccagaagcagcgcgtgagcctggcccgggccgtgtactccaacgctgacatt 2560

Qy   2231 TACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGCAACCACATCTTCAAT 2290
          |||  ||  |  ||  ||  ||||||    ||   |  ||||||||||||||  ||  ||||||||   |
Db   2561 tacctcttcgatgatcccctctcagcagtggatgcccatgtgggaaaacacatctttgaa 2620

Qy   2291 AGTGCTAT------CCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTTACCCACCAG 2344
          |  ||  ||      |  |      ||  |||  ||||||     |  ||  ||  ||  |||
Db   2621 aatgtgattggccccaaggggatgctgaagaacaagacgcggatcttggtcacgcacagc 2680

Qy   2345 TTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGTATTACGGAA 2404
            |   |||  ||     |    ||  |   | |||  ||||||   |  |||    ||  |  ||
Db   2681 atgagctacttgccgcaggtggacgtcatcatcgtcatgagtggcggcaagatctctgag 2740

Qy   2405 AGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATTTTTAATAAC 2464
          |  |||  ||  |  ||||  |||  ||  |  |  |  ||  |  ||  |||    |  |    ||  |
Db   2741 atgggctcctaccaggagctgctggctcgagacggcgccttcgctgagttcctgcgtacc 2800

Qy   2465 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCAAAAAAGGAAACCAGTGGT 2521
                    ||||      ||  |  |    |||   ||        |  ||    |||  |||
Db   2801 tatgccagcacagagcaggagcaggatgcagaggagaacggggtcacgggcgtcagcggt 2860

Qy   2522 TCACAGAAGAAGTCACAAGACAAGG--------GTCCTAAAACAGGATCAATAAAGAAGG 2573
            ||  ||||  |  ||  |  |  ||          |  ||      |||       |  |  |  |
Db   2861 ccagggaaggaagcaaagcaaatggagaatggcatgctggtgacggacagtgcagggaag 2920

Qy   2574 AAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGG---------------------- 2615
            ||  ||||  |   |  ||  |    |  ||  |  ||  ||
Db   2921 caactgcagagacagctcagcagctcctcctcctatagtggggacatcagcaggcaccac 2980

Qy   2616 AAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTG 2675
          ||  ||  |  |       | |||     |||       |  |  ||  |    ||  |  | ||||  ||
Db   2981 aacagcaccgcagaactgcagaaagctgaggccaagaaggaggagacctggaagctgatg 3040

Qy   2676 GGGGC-------CCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGC 2728
          | |||        |   | ||   | |||  |   |  ||  |  |  |    |   |  |
Db   3041 gaggctgacaaggcgcagacagggcaggtcaagctttccgtgtactgggactacatgaag 3100
```

```
Qy   2729 AGCACCGCCTTCAGCACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACC 2788
Db   3101 gccatcggactcttcatctccttcctcagcatcttccttttcatgtgtaaccatgtgtcc 3160

Qy   2789 ACTGTGACT------CGAGGGAACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCT 2842
Db   3161 gcgctggcttccaactattggctcagcctctggactgatgacccccatcgtcaacgggact 3220

Qy   2843 CATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAA 2902
Db   3221 caggagcacacgaaagtccggctgagcgtctatggagccctgggcatttcacaagggatc 3280

Qy   2903 GCCATTCGAGG------AGTTGTCTTTGTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTG 2956
Db   3281 gccgtgtttggctactccatggccgtgtccatcgggggggatcttggcttcccgctgtctg 3340

Qy   2957 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCC 3016
Db   3341 cacgtggacctgctgcacagcatcctgcggtcacccatgagcttctttgagcggacccccc 3400

Qy   3017 ACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCG 3076
Db   3401 agtgggaacctggtgaaccgcttctccaaggagctggacacagtggactccatgatcccg 3460

Qy   3077 TTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATC 3136
Db   3461 gaggtcatcaagatgttcatgggctccctgttcaacgtcattggtgcctgcatcgttatc 3520

Qy   3137 GCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTC 3196
Db   3521 ctgctggccacgcccatcgccgccatcatcatcccgccccttggcctcatctacttcttc 3580

Qy   3197 CTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAG 3256
Db   3581 gtccagaggttctacgtggcttcctcccggcagctgaagcgcctcgagtcggtcagccgc 3640

Qy   3257 TCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTAC 3316
Db   3641 tccccggtctattcccatttcaacgagaccttgctgggggtcagcgtcattcgagccttc 3700

Qy   3317 AATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCT 3376
Db   3701 gaggagcaggagcgcttcatccaccagagtgacctgaaggtggacgagaaccagaaggcc 3760

Qy   3377 TTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATC 3436
Db   3761 tattaccccagcatcgtggccaacaggtggctggccgtgcggctggagtgtgtgggcaac 3820

Qy   3437 GCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCC 3496
Db   3821 tgcatcgttctgtttgctgccctgtttgcggtgatctccaggcacagcctcagtgctggc 3880

Qy   3497 TATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTC 3556
Db   3881 ttggtgggcctctcagtgtcttactcattgcaggtcaccacgtacttgaactggctggtt 3940

Qy   3557 AGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTGGAGAGGATCAATCACTACATT 3616
Db   3941 cggatgtcatctgaaatggaaaccaacatcgtggccgtggagaggctcaaggagtattca 4000

Qy   3617 AAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGG 3676
Db   4001 gagactgagaa---ggaggcgccctggcaaatccaggagacagctccgcccagcagctgg 4057

Qy   3677 CCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATGAGGTACCGAGAAAACCTCCCT 3736
Db   4058 ccccaggtgggccgagtggaattccggaactactgcctgcgctaccgagaggacctggac 4117

Qy   3737 CTCGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAAGAGAAGATTGGCATTGTGGGG 3796
Db   4118 ttcgttctcaggcacatcaatgtcacgatcaatgggggagaaaaggtcggcatcgtgggg 4177

Qy   3797 CGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTCTTCCGTCTGGTGGAGTTATCT 3856
Db   4178 cggacgggagctgggaagtcgtccctgaccctgggcttatttcggatcaacgagtctgcc 4237

Qy   3857 GGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGA 3916
Db   4238 gaaggagagatcatcatcgatggcatcaacatcgccaagatcggcctgcacgacctccgc 4297

Qy   3917 AGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTCAGTGGCACTGTCAGATCAAAT 3976
Db   4298 ttcaagatcaccatcatccccccaggaccctgttttgttttcgggttccctccgaatgaac 4357

Qy   3977 TTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACAC 4036
Db   4358 ctggacccattcagccagtactcggatgaagaagtctggacgtccctggagctggcccac 4417

Qy   4037 ATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGG 4096
Db   4418 ctgaaggacttcgtgtcagcccttcctgacaagctagaccatgaatgtgcagaaggcggg 4477

Qy   4097 GATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
Db   4478 gagaacctcagtgtcgggcagcgccagcttgtgtgcctagcccgggccctgctgaggaag 4537

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
Db   4538 acgaagatccttgtgttggatgaggccacggcagccgtggacctggaaacggacgacctc 4597

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
Db   4598 atccagtccaccatccggacacagttcgaggactgcaccgtcctcaccatcgcccaccgg 4657

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
Db   4658 ctcaacaccatcatggactacacaagggtgatcgtcttggacaaaggagaaatccaggag 4717

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360
Db   4718 tacggcgccccatcggacctcctg 4741
```

RESULT 12
US-09-442-384B-504
; Sequence 504, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 504
; LENGTH: 5011
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-504

Query Match 10.5%; Score 511.2; DB 5; Length 5011;
Best Local Similarity 52.5%; Pred. No. 1.4e-88;
Matches 1367; Conservative 0; Mismatches 1178; Indels 59; Gaps 9;

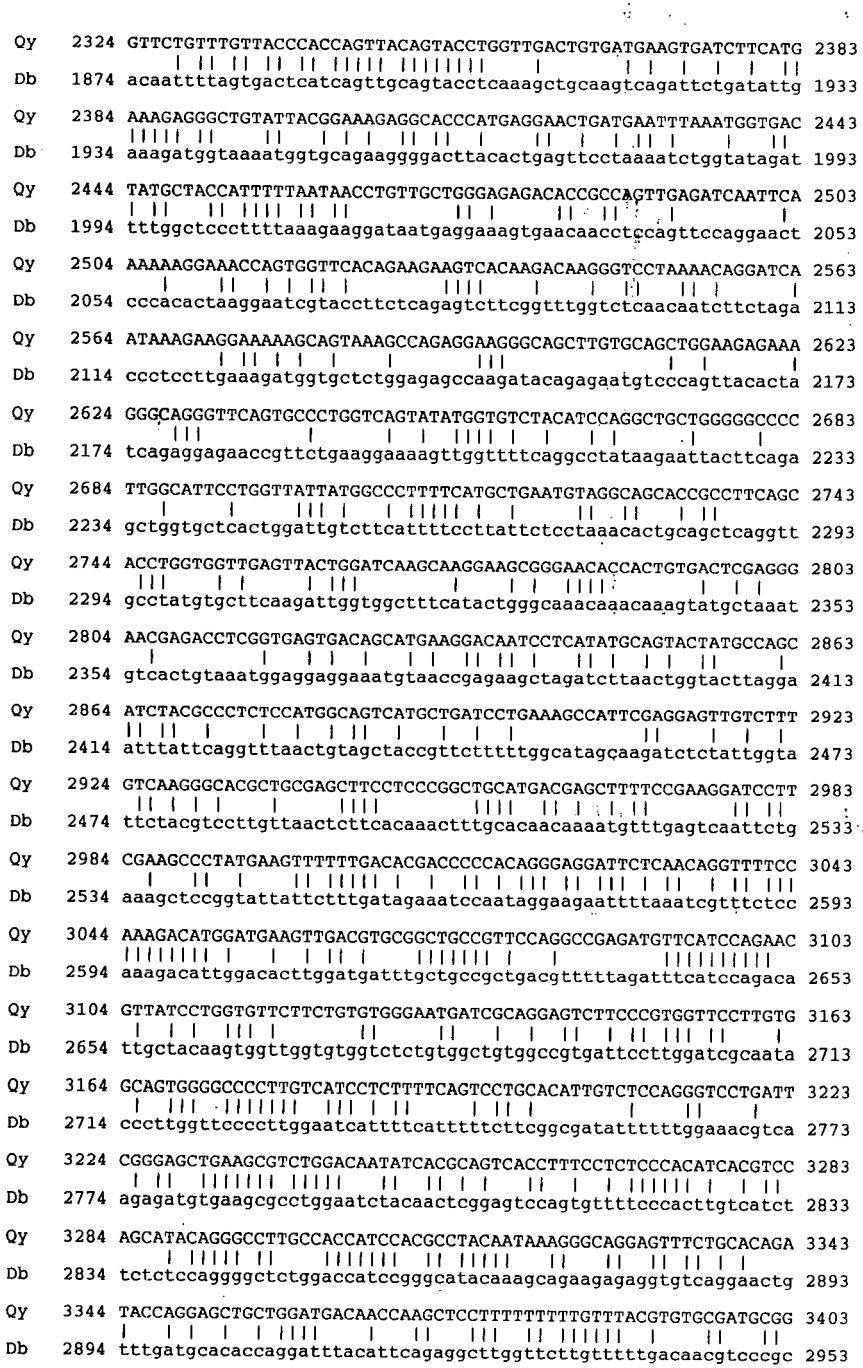
```
Qy   1811 CACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1870
Db   2143 cacattcacctgggcca--ggagcgaccctcccacactgaatggcatcaccttctccatc 2200

Qy   1871 CAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGAAAAACCTCTCTCATT 1930
Db   2201 cccgaaggtgctttggtggccgtggtgggccaggtgggctgcggaaagtcgtccctgctc 2260
```

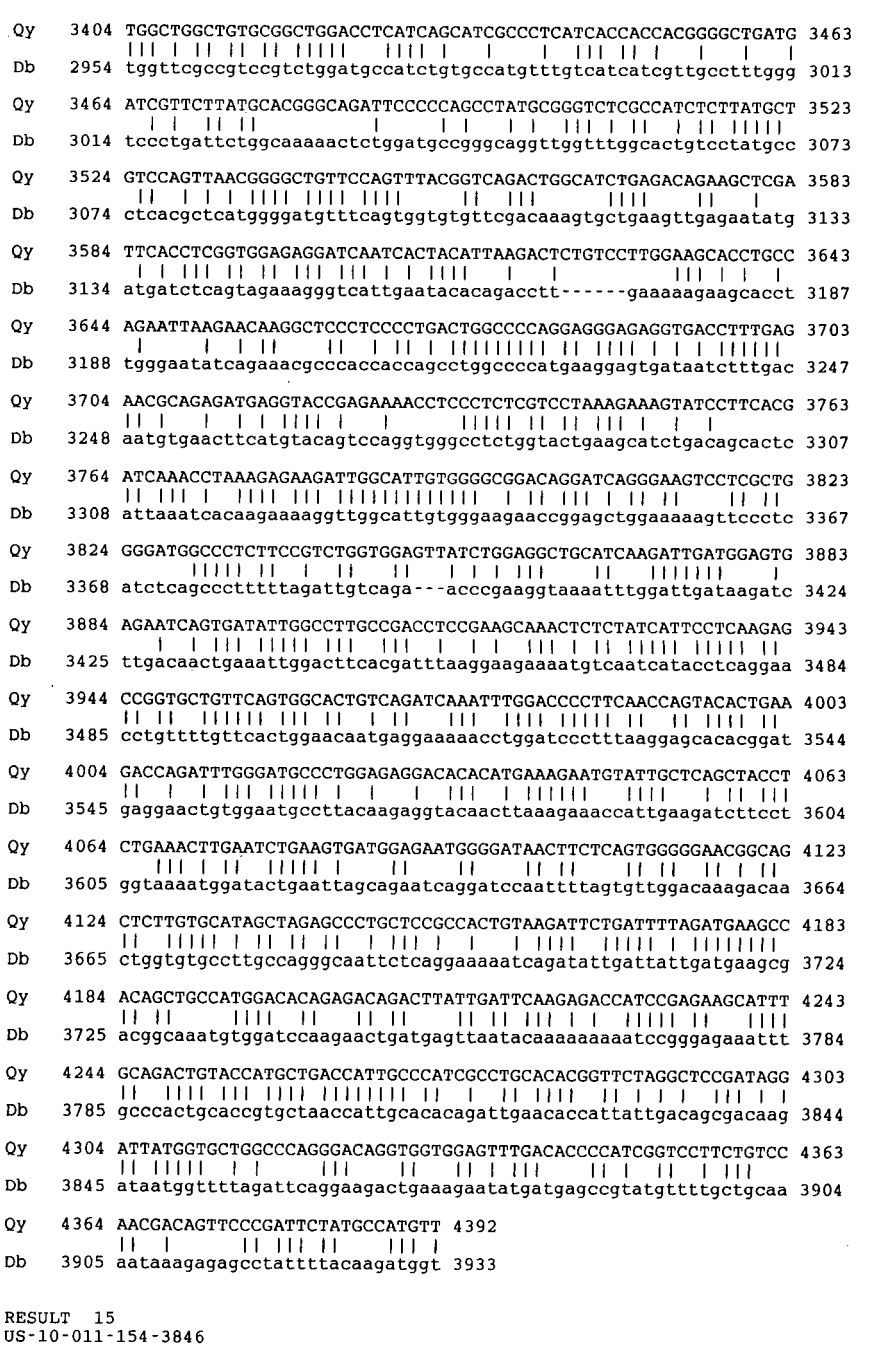
```
Db   4418 ctgaaggacttcgtgtcagcccttcctgacaagctagaccatgaatgtgcagaaggcggg 4477

Qy   4097 GATAACTTCTCAGTGGGGAACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCAC 4156
Db   4478 gagaacctcagtgtcgggcagcgccagcttgtgtgcctagcccgggccctgctgaggaag 4537

Qy   4157 TGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTG 4216
Db   4538 acgaagatccttgtgttggatgaggccacggcagccgtggacctggaaacggacgacctc 4597

Qy   4217 ATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACCATGCTGACCATTGCCCATCGC 4276
Db   4598 atccagtccaccatccggacacagttcgaggactgcaccgtcctcaccatcgcccaccgg 4657

Qy   4277 CTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAG 4336
Db   4658 ctcaacaccatcatggactacacaagggtgatcgtcttggacaaggagaaatccaggag 4717

Qy   4337 TTTGACACCCCATCGGTCCTTCTG 4360
Db   4718 tacggcgccccatcggacctcctg 4741
```

RESULT 13
US-09-930-213-287
; Sequence 287, Application US/09930213
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLNEGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 287
; LENGTH: 4231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-213-287

```
  Query Match            9.0%;  Score 437.4;  DB 5;  Length 4231;
  Best Local Similarity  48.8%;  Pred. No. 2e-74;
  Matches 1244;  Conservative    0;  Mismatches 1296;  Indels    9;  Gaps    2;

Qy   1844 ACACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGT 1903
Db   1394 actctacaaggcctttcctttactgtcagacctggcgaattgttagctgtggtcggcccc 1453

Qy   1904 GTGGGAAGTGGAAAAACCTCTCTCATTTCAGCCATTTAGGCCAGATGACGCTTCTAGAG 1963
Db   1454 gtgggagcagggaagtcatcactgttaagtgccgtgctcggggaattggccccaagtcac 1513

Qy   1964 GGCAGCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAAT 2023
Db   1514 gggctggtcagcgtgcatggaagaattgcctatgtgtctcagcagccctgggtgttctcg 1573

Qy   2024 GCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCT 2083
Db   1574 ggaactctgaggagtaatatttatttgggaagaaatatgaaaaggaacgatatgaaaaa 1633

Qy   2084 GTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACG 2143
Db   1634 gtcataaaggcttgtgctctgaaaaaggatttacagctgttggaggatggtgatctgact 1693

Qy   2144 GAGATTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCC 2203
Db   1694 gtgataggagatcggggaaccacgctgagtggagggcagaaagcacgggtaaaccttgca 1753

Qy   2204 CGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGAT 2263
Db   1754 agagcagtgtatcaagatgctgacatctatctcctggacgatcctctcagtgcagtagat 1813

Qy   2264 GCCCATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACA 2323
Db   1814 gcggaagttagcagacacttgttcgaactgtgtatttgtcaaattttgcatgagaagatc 1873

Qy   2324 GTTCTGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATG 2383
Db   1874 acaattttagtgactcatcagttgcagtacctcaaagctgcaagtcagattctgatattg 1933

Qy   2384 AAAGAGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGAC 2443
Db   1934 aaagatggtaaaatggtgcagaaggggacttacactgagttcctaaaatctggtatagat 1993

Qy   2444 TATGCTACCATTTTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCA 2503
Db   1994 tttggctccctttttaaagaaggataatgaggaaagtgaacaacctccagttccaggaact 2053

Qy   2504 AAAAAGGAAACCAGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCA 2563
Db   2054 cccacactaaggaatcgtaccttctcagagtcttcggtttggtctcaacaatcttctaga 2113

Qy   2564 ATAAAGAAGGAAAAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAA 2623
Db   2114 ccctccttgaaagatggtgctctggagagccaagatacagagaatgtcccagttacacta 2173

Qy   2624 GGGCAGGGTTCAGTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCC 2683
Db   2174 tcagaggagaaccgttctgaaggaaaagttggttttcaggcctataagaattacttcaga 2233

Qy   2684 TTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGC 2743
Db   2234 gctggtgctcactggattgtcttcattttccttattctcctaaacactgcagctcaggtt 2293

Qy   2744 ACCTGGTGGTTGAGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGG 2803
Db   2294 gcctatgtgcttcaagattggtggctttcatactgggcaaacaaacaaagtatgctaaat 2353

Qy   2804 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGC 2863
Db   2354 gtcactgtaaatggaggaggaaatgtaaccgagaagctagatcttaactggtacttagga 2413

Qy   2864 ATCTACGCCCTCTCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTT 2923
Db   2414 atttattcaggtttaactgtagctaccgttctttttggcatagcaagatctctattggta 2473

Qy   2924 GTCAAGGGCACGCTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTT 2983
Db   2474 ttctacgtccttgttaactcttcacaaactttgcacaacaaaatgtttgagtcaattctg 2533

Qy   2984 CGAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCC 3043
Db   2534 aaagctccggtattattctttgatagaaatccaataggaagaattttaaatcgtttctcc 2593

Qy   3044 AAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAAC 3103
Db   2594 aaagacattggacacttggatgatttgctgccgctgacgttttagatttcatccagaca 2653

Qy   3104 GTTATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTG 3163
Db   2654 ttgctacaagtggttggtgtggtctctgtggctgtggccgtgattccttggatcgcaata 2713

Qy   3164 GCAGTGGGGCCCCTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATT 3223
Db   2714 cccttggttccccttggaatcattttcatttttcttcggcgatatttttggaaacgtca 2773
```

```
Qy   3224 CGGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCC 3283
Db   2774 agagatgtgaagcgcctggaatctacaactcggagtccagtgttttcccacttgtcatct 2833

Qy   3284 AGCATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGA 3343
Db   2834 tctctccaggggctctggaccatccgggcatacaaagcagaagagaggtgtcaggaactg 2893

Qy   3344 TACCAGGAGCTGCTGGATGACAACCAAGCTCCTTTTTTTTTGTTTACGTGTGCGATGCGG 3403
Db   2894 tttgatgcacaccaggatttacattcagaggcttggttcttgtttttgacaacgtcccgc 2953

Qy   3404 TGGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATG 3463
Db   2954 tggttcgccgtccgtctggatgccatctgtgccatgtttgtcatcatcgttgcctttggg 3013

Qy   3464 ATCGTTCTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCT 3523
Db   3014 tccctgattctggcaaaaactctggatgccgggcaggttggtttggcactgtcctatgcc 3073

Qy   3524 GTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGA 3583
Db   3074 ctcacgctcatggggatgtttcagtggtgtgttcgacaaagtgctgaagttgagaatatg 3133

Qy   3584 TTCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCC 3643
Db   3134 atgatctcagtagaaagggtcattgaatacacagacctt------gaaaaagaagcacct 3187

Qy   3644 AGAATTAAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAG 3703
Db   3188 tgggaatatcagaaacgcccaccaccagcctggccccatgaaggagtgataatctttgac 3247

Qy   3704 AACGCAGAGATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACG 3763
Db   3248 aatgtgaacttcatgtacagtccaggtgggcctctggtactgaagcatctgacagcactc 3307

Qy   3764 ATCAAACCTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTG 3823
Db   3308 attaaatcacaagaaaaggttggcattgtgggaagaaccggagctggaaaaagttccctc 3367

Qy   3824 GGGATGGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTG 3883
Db   3368 atctcagccctttttagattgtcaga---acccgaaggtaaaatttggattgataagatc 3424

Qy   3884 AGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAG 3943
Db   3425 ttgacaactgaaattggacttcacgatttaaggaagaaaatgtcaatcatacctcaggaa 3484

Qy   3944 CCGGTGCTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAA 4003
Db   3485 cctgttttgttcactggaacaatgaggaaaaacctggatccctttaaggagcacacggat 3544

Qy   4004 GACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCT 4063
Db   3545 gaggaactgtggaatgccttacaagaggtacaacttaaagaaaccattgaagatcttcct 3604

Qy   4064 CTGAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAG 4123
Db   3605 ggtaaaatggatactgaattagcagaatcaggatccaattttagtgttggacaaagacaa 3664

Qy   4124 CTCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCC 4183
Db   3665 ctggtgtgccttgccagggcaattctcaggaaaaatcagatattgattattgatgaagcg 3724

Qy   4184 ACAGCTGCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTT 4243
Db   3725 acggcaaatgtggatccaagaactgatgagttaatacaaaaaaaaatccgggagaaattt 3784

Qy   4244 GCAGACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGG 4303
Db   3785 gcccactgcaccgtgctaaccattgcacacagattgaacaccattattgacagcgacaag 3844

Qy   4304 ATTATGGTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCC 4363
Db   3845 ataatggttttagattcaggaagactgaaagaatatgatgagccgtatgttttgctgcaa 3904

Qy   4364 AACGACAGTTCCCGATTCTATGCCATGTT 4392
Db   3905 aataaagagagcctattttacaagatggt 3933


RESULT  14
US-09-647-140A-1
; Sequence 1, Application US/09647140A
; GENERAL INFORMATION:
;  APPLICANT: Fox Chase Cancer Center
;  APPLICANT:  Kruh, Gary D.
;  APPLICANT:  Lee, Kun
;  APPLICANT:  Belinsky, Martin G.
;  APPLICANT:  Bain, Lisa J.
;  TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
;  TITLE OF INVENTION:  Nucleic Acids and Methods of Use Thereof
;  FILE REFERENCE: FCCC 98-02
;  CURRENT APPLICATION NUMBER: US/09/647,140A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: PCT/US99/06644
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,759
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/095,153
;  PRIOR FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 4231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-647-140A-1


  Query Match             9.0%;  Score 437.4;  DB 5;  Length 4231;
  Best Local Similarity   48.8%;  Pred. No. 2e-74;
  Matches 1244;  Conservative    0;  Mismatches 1296;  Indels    9;  Gaps    2;

Qy   1844 ACACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGT 1903
Db   1394 actctacaaggcctttccttactgtcagacctggcgaattgttagctgtggtcggcccc 1453

Qy   1904 GTGGGAAGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAG 1963
Db   1454 gtgggagcagggaagtcatcactgttaagtgccgtgctcggggaattggccccaagtcac 1513

Qy   1964 GGCAGCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAAT 2023
Db   1514 gggctggtcagcgtgcatggaagaattgcctatgtgtctcagcagccctgggtgttctcg 1573

Qy   2024 GCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCT 2083
Db   1574 ggaactctgaggagtaatattttatttgggaagaaatatgaaaaggaacgatatgaaaaa 1633

Qy   2084 GTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACG 2143
Db   1634 gtcataaaggcttgtgctctgaaaaaggatttacagctgttggaggatggtgatctgact 1693

Qy   2144 GAGATTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCC 2203
Db   1694 gtgataggagatcggggaaccacgctgagtggagggcagaaagcacgggtaaaccttgca 1753

Qy   2204 CGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGAT 2263
Db   1754 agagcagtgtatcaagatgctgacatctatctcctggacgatcctctcagtgcagtagat 1813

Qy   2264 GCCCATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACA 2323
Db   1814 gcggaagttagcagacacttgttcgaactgtgtatttgtcaaattttgcatgagaagatc 1873
```





RESULT 15
US-10-011-154-3846
; Sequence 3846, Application US/10011154
; GENERAL INFORMATION:

```
;  APPLICANT: Drmanac, Radoje T.
;  APPLICANT:  Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Dickson, Mark C.
;  APPLICANT:  Jones, Lee w.
;  TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION:  From Various Libraries
;  FILE REFERENCE: 780CIP
;  CURRENT APPLICATION NUMBER: US/10/011,154
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038
;  PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
;  NUMBER OF SEQ ID NOS: 4670
;  SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 3846
;   LENGTH: 426
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-011-154-3846

  Query Match             8.5%;  Score 409.8;  DB 7;  Length 426;
  Best Local Similarity   99.5%;  Pred. No. 2.9e-69;
  Matches  411;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   4073 GAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGC 4132
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     14 gaggctgaagtgatggagaatggggataacttctcagtgggggaacggcagctcttgtgc 73

Qy   4133 ATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCC 4192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 atagctagagccctgctccgccactgtaagattctgattttagatgaagccacagctgcc 133

Qy   4193 ATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGT 4252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 atggacacagagacagacttattgattcaagagaccatccgagaagcatttgcagactgt 193

Qy   4253 ACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTG 4312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 accatgctgaccattgcccatcgcctgcacacggttctaggctccgataggattatggtg 253

Qy   4313 CTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGT 4372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 ctggcccagggacaggtggtggagtttgacaccccatcggtccttctgtccaacgacagt 313

Qy   4373 TCCCGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGACTC 4432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 tcccgattctatgccatgtttgctgctgcagagaacaaggtcgctgtcaagggctgactc 373

Qy   4433 CTCCCTGTTGACGAAGTCTCTTTTCTTTAGAGCATTGCCATTCCCTGCCTGGG 4485
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 ctccctgttgacgaagtctcttttctttagagcattgccattccctgcctggg 426


Search completed: August 11, 2002, 11:11:20
Job time: 6765 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 11, 2002, 09:20:05 ; Search time 25.86 Seconds
(without alignments)
1357.292 Million cell updates/sec

Title: US-09-528-031-2
Perfect score: 7308
Sequence: 1 MKDIDIGKEYIIPSPGYRSV.....DSSRFYAMFAAAENKVAVKG 1437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7308	100.0	1437	3	US-09-061-400-2	Sequence 2, Appli
2	7298	99.9	1453	2	US-09-001-273-2	Sequence 2, Appli
3	7298	99.9	1453	4	US-08-843-459A-2	Sequence 2, Appli
4	2082	28.5	1531	1	US-08-463-092B-4	Sequence 4, Appli
5	2082	28.5	1531	2	US-08-462-109A-4	Sequence 4, Appli
6	2082	28.5	1531	2	US-08-460-907B-4	Sequence 4, Appli
7	2082	28.5	1531	3	US-08-463-179A-4	Sequence 4, Appli
8	2082	28.5	1531	3	US-08-461-384B-4	Sequence 4, Appli
9	2075	28.4	1531	1	US-08-141-893-2	Sequence 2, Appli
10	2075	28.4	1531	1	US-08-463-092B-2	Sequence 2, Appli
11	2075	28.4	1531	2	US-08-462-109A-2	Sequence 2, Appli
12	2075	28.4	1531	2	US-08-460-907B-2	Sequence 2, Appli
13	2075	28.4	1531	3	US-08-463-179A-2	Sequence 2, Appli
14	2075	28.4	1531	3	US-08-461-384B-2	Sequence 2, Appli
15	2075	28.4	1531	3	US-08-407-207A-2	Sequence 2, Appli
16	2055.5	28.1	1528	1	US-08-463-092B-6	Sequence 6, Appli
17	2055.5	28.1	1528	2	US-08-462-109A-6	Sequence 6, Appli
18	2055.5	28.1	1528	2	US-08-460-907B-6	Sequence 6, Appli
19	2055.5	28.1	1528	3	US-08-463-179A-6	Sequence 6, Appli
20	2055.5	28.1	1528	3	US-08-461-384B-6	Sequence 6, Appli
21	2013.5	27.6	1622	4	US-08-972-927-6	Sequence 6, Appli
22	2006	27.4	1261	4	US-09-439-313-538	Sequence 538, App
23	1991	27.2	1621	4	US-08-972-927-3	Sequence 3, Appli
24	1894.5	25.9	1228	4	US-09-439-313-537	Sequence 537, App
25	1759	24.1	1581	4	US-08-726-320-3	Sequence 3, Appli
26	1759	24.1	1581	4	US-09-208-716-3	Sequence 3, Appli
27	1757.5	24.0	1580	4	US-08-726-320-1	Sequence 1, Appli
28	1757.5	24.0	1580	4	US-09-208-716-1	Sequence 1, Appli
29	1732	23.7	1581	4	US-08-726-320-4	Sequence 4, Appli
30	1732	23.7	1581	4	US-09-208-716-4	Sequence 4, Appli
31	1730	23.7	1477	3	US-08-492-459-10	Sequence 10, Appl
32	1730	23.7	1477	3	US-08-423-752-10	Sequence 10, Appl
33	1730	23.7	1477	3	US-08-945-994-3	Sequence 3, Appli
34	1730	23.7	1477	4	US-08-716-873-24	Sequence 24, Appl
35	1730	23.7	1477	4	US-09-368-431-24	Sequence 24, Appl
36	1730	23.7	1477	4	US-09-414-006-10	Sequence 10, Appl
37	1669.5	22.8	1581	2	US-08-404-531B-6	Sequence 6, Appli
38	1669.5	22.8	1581	3	US-08-476-900A-6	Sequence 6, Appli
39	1669.5	22.8	1581	3	US-08-488-546A-6	Sequence 6, Appli
40	1669.5	22.8	1582	2	US-08-404-531B-9	Sequence 9, Appli
41	1669.5	22.8	1582	3	US-08-476-900A-9	Sequence 9, Appli
42	1669.5	22.8	1582	3	US-08-488-546A-9	Sequence 9, Appli
43	1669.5	22.8	1582	4	US-08-726-320-5	Sequence 5, Appli
44	1669.5	22.8	1582	4	US-09-208-716-5	Sequence 5, Appli
45	1528.5	20.9	1498	2	US-08-404-531B-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-061-400-2
; Sequence 2, Application US/09061400
; Patent No. 6077936
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,400
; FILING DATE: 16-APRIL-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-056CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-061-400-2

Query Match 100.0%; Score 7308; DB 3; Length 1437;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
```

```
Db      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Db     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Db     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
Db     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Db     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Db     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
Db     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Db     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Db     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Db     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
Db     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840

Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
Db     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
Db     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
Db     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
Db    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
Db    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
```

```
Db    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
Db    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
Db    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
Db    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
Db    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
```

RESULT 2
US-09-001-273-2
; Sequence 2, Application US/09001273
; Patent No. 5994130
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibeault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,273
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON, Gillian M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-273-2

Query Match 99.9%; Score 7298; DB 2; Length 1453;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Db     17 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 76

Qy     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
Db     77 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 136

Qy    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
```

```
Db    137 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 196

Qy    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Db    197 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 256

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Db    257 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 316

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Db    317 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 376

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Db    377 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 436

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Db    437 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 496

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Db    497 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 556

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Db    557 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 616

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Db    617 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 676

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Db    677 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 736

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Db    737 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 796

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840

Db    797 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 856

Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Db    857 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 916

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Db    917 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 976

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Db    977 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1036

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Db   1037 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1096

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Db   1097 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1156

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Db   1157 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1216

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Db   1217 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1276

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Db   1277 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1336

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Db   1337 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1396

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437

Db   1397 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1453
```

RESULT 3
US-08-843-459A-2
; Sequence 2, Application US/08843459A
; Patent No. 6162616
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,459A
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-056 (formerly MIL-001)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-843-459A-2

Query Match 99.9%; Score 7298; DB 4; Length 1453;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Db     17 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 76

Qy     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120

Db     77 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 136

Qy    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Db    137 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 196

Qy    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
```

```
Db    197 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 256

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Db    257 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 316

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Db    317 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 376

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Db    377 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 436

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Db    437 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 496

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Db    497 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 556

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Db    557 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 616

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Db    617 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 676

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Db    677 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 736

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Db    737 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 796

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840

Db    797 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 856

Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Db    857 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 916

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Db    917 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 976

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Db    977 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1036

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Db   1037 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1096

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Db   1097 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1156

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Db   1157 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1216

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Db   1217 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1276

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Db   1277 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1336

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Db   1337 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1396

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437

Db   1397 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1453
```

RESULT 4
US-08-463-092B-4
; Sequence 4, Application US/08463092B
; Patent No. 5766880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,092B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-0CT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-0CT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1531 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-092B-4

Query Match 28.5%; Score 2082; DB 1; Length 1531;
Best Local Similarity 34.5%; Pred. No. 2.5e-195;
Matches 488; Conservative 262; Mismatches 479; Indels 184; Gaps 21;

```
Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA---------------------------SLRRVVWIFCRTRLIL 181
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW---------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
Db    654 ----------------------ARSDPP----------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
Db    676 VVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF----------------------------------NNLLL----GETPPVEIN 795
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
Db   1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETAPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db   1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db   1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db   1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db   1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524
```

RESULT 5
US-08-462-109A-4
; Sequence 4, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1531 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-109A-4

```
  Query Match             28.5%;  Score 2082;  DB 2;  Length 1531;
  Best Local Similarity   34.5%;  Pred. No. 2.5e-195;
  Matches  488;  Conservative  262;  Mismatches  479;  Indels  184;  Gaps   21;

Qy     100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
Db     209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy     160 V----------GPDAA--------------------------SLRRVVWIFCRTRLIL 181
Db     268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy     182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
Db     328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy     242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
Db     387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy     300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
Db     447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy     360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
Db     507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy     420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
Db     567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy     478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
Db     627 PDSIERRPVKDGGGTNSITVRNATFTW---------------------------------- 653

Qy     533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
Db     654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy     593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
Db     676 VVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy     653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
Db     736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy     713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db     796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy     771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
Db     856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy     796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
Db     916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy     856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
Db     973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy     916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
Db    1029 AVFGYSMAVSI------------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy     976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
Db    1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy    1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
Db    1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy    1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
Db    1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy    1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db    1254 METNIVAVERLKEYSET-EKEAPWQIQETAPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy    1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db    1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy    1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db    1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy    1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db    1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy    1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db    1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524
```

```
RESULT   6
US-08-460-907B-4
; Sequence 4, Application US/08460907B
; Patent No. 5891724
;  GENERAL INFORMATION:
;    APPLICANT:  Deeley, Roger G.
;    APPLICANT:  Cole, Susan P.C.
;    TITLE OF INVENTION:  METHODS FOR CONFERRING MULTIDRUG
;    TITLE OF INVENTION:  RESISTANCE ON A CELL
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,907B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1551
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-460-907B-4


  Query Match           28.5%;  Score 2082;  DB 2;  Length 1531;
  Best Local Similarity   34.5%;  Pred. No. 2.5e-195;
  Matches  488;  Conservative  262;  Mismatches  479;  Indels  184;  Gaps   21;

Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA--------------------------SLRRVVWIFCRTRLIL 181
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW---------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
Db    654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
Db    676 VVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855

Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
Db   1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETAPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db   1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db   1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db   1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db   1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT   7
US-08-463-179A-4
; Sequence 4, Application US/08463179A
; Patent No. 6001563
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING CHEMOSENSITIZERS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,179A
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-0CT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
```

```
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002CP8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-463-179A-4
```

Query Match 28.5%; Score 2082; DB 3; Length 1531;
Best Local Similarity 34.5%; Pred. No. 2.5e-195;
Matches 488; Conservative 262; Mismatches 479; Indels 184; Gaps 21;

```
Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA--------------------------SLRRVVWIFCRTRLIL 181
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW---------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
Db    654 ----------------------ARSDPP----------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
Db    676 VVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
```

```
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
Db    1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
Db    1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy    1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
Db    1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy    1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
Db    1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy    1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db    1254 METNIVAVERLKEYSET-EKEAPWQIQETAPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy    1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db    1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy    1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db    1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy    1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db    1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy    1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db    1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524
```

```
RESULT   8
US-08-461-384B-4
; Sequence 4, Application US/08461384B
; Patent No. 6025473
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEINS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,384B
;      FILING DATE:  05-JUN-95
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1547
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-384B-4


  Query Match             28.5%;  Score 2082;  DB 3;  Length 1531;
  Best Local Similarity   34.5%;  Pred. No. 2.5e-195;
  Matches  488;  Conservative  262;  Mismatches  479;  Indels  184;  Gaps   21;

Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA---------------------------SLRRVVWIFCRTRLIL 181
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW---------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
Db    654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
Db    676 VVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
```

```
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF----------------------------NNLLL----GETPPVEIN 795
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
Db   1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETAPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db   1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db   1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db   1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db   1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT   9
US-08-141-893-2
; Sequence 2, Application US/08141893
; Patent No. 5489519
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEIN
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/141,893
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923; 08/029,340
;      FILING DATE:  27-OCT-1992; 8-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5149
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-141-893-2


  Query Match             28.4%;  Score 2075;  DB 1;  Length 1531;
  Best Local Similarity   34.5%;  Pred. No. 1.2e-194;
  Matches  487;  Conservative  261;  Mismatches  481;  Indels  184;  Gaps   21;

Qy     100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
           |  :|   | :|| |:: |  |   :  |   |:|||:| ::|:     | : |::|  :
Db     209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy     160 V----------GPDAA--------------------------SLRRVVWIFCRTRLIL 181
                      | |                          || :|::       ::
Db     268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy     182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
           |     |  |  ||||  ::| |:::   |::         : |:: |  :::  |   :
Db     328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy     242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
           : : :|:|:: |::   ::| | : |   ||  :||::|: |:||| : |   :::
Db     387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy     300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
            |:  || :   : |||:  | || :|  |    :  |  :  : : | |:: ||
Db     447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy     360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
           |:|  || :|:|||  ||    |  ||:|| ::|:|: |  ::          : :: ||:
Db     507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy     420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
           |::|:  :  | |  ||  : :|| : | | : |  : |: :|||:: | :     ||:
Db     567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy     478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
             |: :|         | ::|||  |
Db     627 PDSIERRPVKDGGGTNSITVRNATFTW------------------------------- 653

Qy     533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
                                   | |                 ||: |   | || ||
Db     654 ---------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy     593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
           : | || || ||:||:| :|  :|| :|| |: ||| ||||| | :||:|||| : :|
Db     676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy     653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
            | ||: :| | ||| |||| | |||||:| ||||||:||:|||||:||:  ||: ||||
Db     736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy     713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
           ||:|||| ||| : |  :  ||:|| : ||| : ||   | :| |  | |:| |:::||

Db     796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy     771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
           :  :| :|                                  | :|:    |:    :::
Db     856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy     796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
           |    ||   :  :    |  ::| :| | |  :|:: ::   | |  |||  |::| |
Db     916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy     856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
            ::|| |  ||| |  |   | :||| |       | |      | |  |:     :
Db     973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy     916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
           :::  |||| :           | : ||  || :|   ||||| ||: ||:| ::|||
Db    1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy     976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
           ||::| ||  :|   :||: ::  |    :|    |   : : || :::      | |
Db    1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy    1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
           :   |:||||:::::|| ||   :: |:: | |: : : |:|:    :|:||  ::
Db    1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy    1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
           | |||||||: :   ::    |  |:    :     ||::||::|:|    : ||::||
Db    1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy    1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
           |    :|||:  | :|   ||| :|:    |  ||| | | | | :||||:|  ||:
Db    1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy    1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
           :: ||   ||:|||||||:|||| : |||: | : | | |||: |: ||| ||| |::|
Db    1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy    1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
           |||:|||||::| |||||:||:::::| :||  |:|: :: || ||: |  | |:| ||
Db    1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy    1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
           |:|||:|:|||||  |||:|||||||:| ||| ||| |||  | |||:|||||||:|::
Db    1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy    1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
              |::|| :|:: |:  || ||      ||:|
Db    1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT  10
US-08-463-092B-2
; Sequence 2, Application US/08463092B
; Patent No. 5766880
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULES ENCODING
;    TITLE OF INVENTION:  MULTIDRUG RESISTANCE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,092B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1546
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-463-092B-2


  Query Match           28.4%;  Score 2075;  DB 1;  Length 1531;
  Best Local Similarity  34.5%;  Pred. No. 1.2e-194;
  Matches  487;  Conservative  261;  Mismatches  481;  Indels  184;  Gaps   21;

Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA----------------------------SLRRVVWIFCRTRLIL 181
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW---------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592

Db    654 ----------------------ARSDPP----------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
Db    676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
Db   1029 AVFGYSMAVSI------------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db   1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db   1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db   1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db   1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT  11
US-08-462-109A-2
; Sequence 2, Application US/08462109A
; Patent No. 5882875
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING
;    TITLE OF INVENTION:  MULTIDRUG RESISTANT TUMOR CELLS
```

```
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,109A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002CP4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-109A-2


  Query Match             28.4%;  Score 2075;  DB 2;  Length 1531;
  Best Local Similarity   34.5%;  Pred. No. 1.2e-194;
  Matches  487;  Conservative  261;  Mismatches  481;  Indels  184;  Gaps   21;

Qy     100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
           |  :|    | :|| |:: |  |    :  |   |:|||:| ::|:     | : |::|  :
Db     209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy     160 V----------GPDAA---------------------------SLRRVVWIFCRTRLIL 181
                       | |                          :|| :|:::    :    ::
Db     268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy     182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
           |     |  |  ||||  ::| |:::   |::          : | :|  :::  |   :
Db     328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy     242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
           : : :|:|:: |::   ::| | : |   ||  :||::|: | | ||  : |   :::
Db     387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy     300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
             |:  || :    : |||:   | || :|  |     :  |  ::   : : | |:: ||
Db     447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy     360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
           |:|  || :|:|||  ||   |  ||:|| ::|:|: |  ::          : :: ||:
Db     507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy     420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
           |::|:  :  | |  ||  : :|| : | | : |  : |: :|||:: | :     ||:
Db     567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy     478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
             |: :|         | ::|||  |
Db     627 PDSIERRPVKDGGGTNSITVRNATFTW------------------------------ 653

Qy     533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
                                   |  |                  ||: |   | || ||
Db     654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy     593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
           : | || || ||:||:| :|  :|| :|| |: ||| ||||| | :|||:||||| : :|
Db     676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy     653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
             | ||: :| | ||| |||| | |||||:| ||||||:||:|||||:||:  ||: ||||
Db     736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy     713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
           ||:||||| ||| : |  :  ||:|| : ||| : ||   | :| |  | |:| |:::||
Db     796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy     771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
           :  :| :|                                  | :|:    |:    :::
Db     856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy     796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
           |    ||   :  :    | ::| :| | |  :|:: ::   | |  |||  |::| |
Db     916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy     856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
           ::|| |  ||| | |   | :||| |       | |       | |  |:    :
Db     973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy     916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
           :::  |||| :             | : ||  || :|   |||||| ||: ||:| ::|||
Db    1029 AVFGYSMAVSI------------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy     976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
           ||::| ||  :|  :||: ::  |     :|    |   : : || :::     | |
Db    1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy    1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
           :  |:||||::::|| ||   :: |:: | |: : : |:|:    :|:||  ::
Db    1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy    1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
             | |||||||: :   ::    |  |:    :     ||::||::|:|    : ||::||
Db    1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy    1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
           |    :|||:  | :|   ||| :|:   |   ||| | | | |  :||||:|  ||:
Db    1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy    1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
           :: ||   ||:|||||||:|||||  : |||: | : | | |||: |: ||| ||| |:|
Db    1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy    1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
           |||:||||||::| |||||:||:::::| :||  |:|: :: || ||: |  | |:| ||
Db    1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy    1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
           |:|||:|:|||||  |||:||||||:| ||| ||| |||  | |||:|||||||:|::
Db    1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy    1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
             |::|| :|:: |:  || ||      ||:|
Db    1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT  12
US-08-460-907B-2
; Sequence 2, Application US/08460907B
```

```
; Patent No. 5891724
;  GENERAL INFORMATION:
;    APPLICANT:  Deeley, Roger G.
;    APPLICANT:  Cole, Susan P.C.
;    TITLE OF INVENTION:  METHODS FOR CONFERRING MULTIDRUG
;    TITLE OF INVENTION:  RESISTANCE ON A CELL
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,907B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1551
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-460-907B-2


  Query Match           28.4%;  Score 2075;  DB 2;  Length 1531;
  Best Local Similarity  34.5%;  Pred. No. 1.2e-194;
  Matches  487;  Conservative  261;  Mismatches  481;  Indels  184;  Gaps   21;

Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
          |  :|   | :|| |:: |  |   :  |   |:|||:| ::|:    | : |::|  :
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA-------------------------SLRRVVWIFCRTRLIL 181
                       | |                         || :|::      ::
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
          |     |  |  ||||  ::| |:::   |::          : | :|  ::: |   :
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
          : : :|:|:: |::   ::| | : |   ||  :||::|: | | ||  : |   :::

Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
          |:  || :    : |||:   | || :|  |      :  |  ::   : : | |:: ||
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
          |:|  || :|:|||  ||   |  ||:|| ::|:|: |  ::          : :: ||:
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
          |::|:  :  | |  ||  : :|| : | | : |  : |: :|||:: | :     ||:
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
             |: :|         | ::|||  |
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
                                      |  |                  ||: |   | || ||
Db    654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
          : | || || ||:||:| :|  :|| :|| |: ||| ||||| | :||:|||| : :|
Db    676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
          | ||: :| | ||| |||| | |||||:| ||||||:||:|||||:||:  ||: ||||
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
          ||:||||| ||| : |  :  ||:|| : ||| : ||   | :| |  | |:| |::||
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF--------------------------------NNLLL----GETPPVEIN 795
          :  :| :|                                   | :|:    |:    :::
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
          |    ||   :  :    |  ::| :| | |  :|:: ::   | |  |||  |::| |
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
          ::|| |  ||| |  |   | :||| |      | |      | |   |:    :
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
          :::  |||| :           | : ||  || :|  ||||| ||: ||:| ::|||
Db   1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
          ||::| ||  :|   :||: ::  |     :|    |   : : || :::     | |
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
          :   |:||||:::::||  ||   :: |:: | |: : : |:|:    :|:||  ::
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
          | |||||||: :   ::    |  |:    :     ||::||::|:|    : ||::||
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
          |    :|||:  | :|   ||| :|:   |   ||| | | | |  :||||:|  ||:
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
          :: ||   ||:|||||||:|||| : |||: | : | | |||: |: ||| ||| |::|
Db   1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
          |||:|||||::| |||||:||:::::| :||  |:|: :: || ||: |  | |:| ||
Db   1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432
```

```
Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
          |:|||:|:|||||  |||:||||||:| ||| ||| |||  | |||:|||||||:|::
Db   1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
             |::|| :|:: |:  || ||      ||:|
Db   1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT 13
US-08-463-179A-2
; Sequence 2, Application US/08463179A
; Patent No. 6001563
;  GENERAL INFORMATION:
;    APPLICANT:  Cole, Susan P.C.
;    APPLICANT:  Deeley, Roger G.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING CHEMOSENSITIZERS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,179A
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;      APPLICATION NUMBER:  08/407,207
;      FILING DATE:  20-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A. Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  PQI-002CP8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-463-179A-2


  Query Match             28.4%;  Score 2075;  DB 3;  Length 1531;
  Best Local Similarity   34.5%;  Pred. No. 1.2e-194;
  Matches  487;  Conservative  261;  Mismatches  481;  Indels  184;  Gaps   21;

Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
          |  :|   | :|| |:: |  |   :  |   |:|||:| ::|:     | : |::|  :
Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA---------------------------SLRRVVWIFCRTRLIL 181
                       | |                          || :|::       ::
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241

Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
          : : :|:|:: |::   ::| | : |   ||  :||::|: | | ||  : |   :::
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
           |:  || :    : |||:   | || :|  |     :  | ::   : : | |:: ||
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
          |:|  || :|:|||  ||   |  ||:|| ::|:|: |  ::          : :: ||:
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
          |::|:  :  | |  ||  : :|| : | | : |  : |: :|||:: | :     ||:
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
            |: :|         | ::|||  |
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW-------------------------------- 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
                                    | |                  ||: |   | || ||
Db    654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
          : | || || ||:||:| :|  :|| :|| |: ||| ||||| | :||:|||| : :|
Db    676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
           | ||: :| | ||| |||| | |||||:| ||||||:||:|||||:||:  ||: ||||
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
          ||:|||| ||| : |  :  ||:|| : ||| : ||   | :| |  | ||:| |:::||
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF-------------------------------NNLLL----GETPPVEIN 795
          :  :| :|                                   | :|:    |:    :::
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
          |   ||   :  :    | ::| :| | |  :|:: ::   | |  |||  |::| |
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
           ::|| |  ||| |  |   | :||| |      | |      | |  |:     :
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
          :::  |||| :            | : ||  || :|   |||||| ||: ||:| ::|||
Db   1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
          ||::| ||  :|   :||: ::  |     :|    |   : : || :::     | |
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
          :  |:||||:::::||  ||   :: |:: | |: : : |:|:    :|:||  ::
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
           | |||||||: :   ::    |  |:    :     ||::||::|:|    : ||::||
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
           |    :|||:  | :|   ||| :|:   |   ||| | | | |  :||||:|  ||:
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
          :: ||   ||:|||||||:||||| : |||: | : | | |||: |: ||| ||| |::|
```

```
Db     1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIDGINIAKIGLHDLRFKITI 1372

Qy     1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
            |||:||||||::| |||||:|:::::| :||  |:|: :: || ||: |  | |:| ||
Db     1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKEDHECAEGGENLSV 1432

Qy     1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
            |:|||:|:||||||  |||:||||||||:| ||| ||| |||  | |||:|||||||:|::
Db     1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy     1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
                |::|| :|:: |:  || ||      ||:|
Db     1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524
```

RESULT 14
US-08-461-384B-2
; Sequence 2, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1531 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-384B-2

Query Match 28.4%; Score 2075; DB 3; Length 1531;
Best Local Similarity 34.5%; Pred. No. 1.2e-194;
Matches 487; Conservative 261; Mismatches 481; Indels 184; Gaps 21;

```
Qy      100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
            |  :|   | :|| |:: |  |    :  |   |:|||:| ::|:      | : |::|  :
Db      209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy      160 V----------GPDAA---------------------------SLRRVVWIFCRTRLIL 181
                       | |                                   || :|::      ::
Db      268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy      182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
            |     |  |  ||||  ::| |:::   |::              : | :|  ::: |   :
Db      328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy      242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
            : : :|:|:: |::   ::| |  : |    ||  :||::|: | | ||   : |    :::
Db      387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy      300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
             |:  ||  :      : |||:   | || :|  |       :   |   ::   : : | |:: ||
Db      447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy      360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
            |:|  || :|:||| ||    |   ||:|| ::|:|:  | ::              : :: ||:
Db      507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy      420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
            |::|:  :   | |  ||   : :||  : |  | :  |  : |: :|||:: | :      ||:
Db      567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy      478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
                |: :|           | ::|||  |
Db      627 PDSIERRPVKDGGGTNSITVRNATFTW--------------------------------- 653

Qy      533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
                                  |  |                   ||:  |   | || ||
Db      654 ----------------------ARSDPP----------------TLNGITFSIPEGALVA 675

Qy      593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
             : | || || ||:||:| :|  :|| :|| |: ||| ||||| | :||:||||| : :|
Db      676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy      653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
             | ||: :| | ||| |||| | |||||:| |||||:||:||||||:||:  ||: ||||
Db      736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy      713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
            ||:||||| ||| : |   :  ||:|| : |||  :  ||    | :| |   | |:| |:::||
Db      796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy      771 MNLNGDYATIF-----------------------------NNLLL----GETPPVEIN 795
             :  :| :|                                  | :|:     |:      :::
Db      856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy      796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
             |   ||    :    :     |   ::|  :| | |  :|:: ::   | |   |||  |::| |
Db      916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy      856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
             ::|| |  ||| |   |   | :||| |          | |           | |  |:      :
Db      973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy      916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
            ::: ||||  :             | : ||  || :|   ||||| ||: ||:| ::|||
Db     1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy      976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
            ||::|| ||  :|     :||: :|  ::  :|     :|   |   : :|:   : || :::   ||
Db     1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy     1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
             :   |:||||:::::|| ||    :: :|::  |  |: : :  |:|:     :|:||  ::
Db     1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy     1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
             | |||||||: :    ::      |  |:     :       ||::||::|:|     : ||::||
Db     1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253

Qy     1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
              |    :|||:  | :|   ||| :|:     |     ||| | | | |  :||||:|  ||:
```

```
Db   1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
          ::|||   ||:|||||||:||||| : |||: | : | | |||: |: ||| ||| |::|
Db   1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
          |||:||||||::| |||||:||:::::| :||  |:|: :: || ||: |  | |:| ||
Db   1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
          |:|||:|:|||||  |||:||||||:| ||| ||| |||  | |||:||||||:|::
Db   1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
          |::|| :|:: |:  || ||      ||:|
Db   1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524


RESULT 15
US-08-407-207A-2
; Sequence 2, Application US/08407207A
; Patent No. 6063621
;  GENERAL INFORMATION:
;    APPLICANT:  Deeley, Roger G.
;    APPLICANT:  Cole, Susan P.C.
;    TITLE OF INVENTION:  ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
;      STREET:  Queen's University at Kingston
;      CITY:  Kingston
;      STATE:  Ontario
;      COUNTRY:  CANADA
;      ZIP:  K7L 3N6
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/407,207A
;      FILING DATE:  20-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/966,923
;      FILING DATE:  27-OCT-1992
;      APPLICATION NUMBER:  08/029,340
;      FILING DATE:  8-MAR-1993
;      APPLICATION NUMBER:  08/141,893
;      FILING DATE:  26-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steeg, Carol Miernicki
;      REGISTRATION NUMBER:  39,539
;      REFERENCE/DOCKET NUMBER:  Q1512
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (613) 545-2342
;      TELEFAX:  (613) 545-6853
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1531 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-407-207A-2


  Query Match           28.4%;  Score 2075;  DB 3;  Length 1531;
  Best Local Similarity  34.5%;  Pred. No. 1.2e-194;
  Matches 487;  Conservative  261;  Mismatches  481;  Indels  184;  Gaps   21;

Qy    100 PVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNE 159
          |  :|   | :|| |:: |  |   :  |   |:|||:| ::|:     | : |::|  :

Db    209 PESSASFLSRITFWWITGLI-VRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAK 267

Qy    160 V----------GPDAA--------------------------SLRRVVWIFCRTRLIL 181
                       | |                          || :|:: ::
Db    268 TRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIVKSPQKEWNPSLFKVLYKTFGPYFLM 327

Qy    182 SIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWA 241
          |     |  |  |||| ::| |:::   |::          : | :|  :::  |   :
Db    328 SFFFKAIHDLMMFSGPQ-ILKLLIKFVNDTKAPDWQGYFYTVLLFVTACLQTLVLHQYFH 386

Qy    242 LNYRTGVRLRGAILTMAFKKILKLKNIKEKS--LGELINICSNDGQRMFEAAAVGSLLAG 299
          : : :|:|:: |::   ::| | : |   ||  :||::|: | | ||  : |   :::
Db    387 ICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWS 446

Qy    300 GPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMN 359
           |:  || :    : |||:   | || :|  |      :  |  ::   : : | |:: ||
Db    447 APLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHMKSKDNRIKLMN 506

Qy    360 EVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFS 419
          |:|  || :|:||| ||   |  ||:|| ::|:|: |  ::          : :: ||:
Db    507 EILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFA 566

Qy    420 VHMTLGFD--LTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVH 477
          |::|:  :  | |  ||  : :|| : | | : |  : |: :|||:: | :    ||:
Db    567 VYVTIDENNILDAQTAFVSLALFNILRFPLNILPMVISSIVQASVSLKRLRIFLSHEELE 626

Qy    478 --MIKNKPASP---HIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQ 532
            |: :|       | ::|||  |
Db    627 PDSIERRPVKDGGGTNSITVRNATFTW------------------------------ 653

Qy    533 LQRTEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVG 592
                                  |  |                 ||: |   | || ||
Db    654 ----------------------ARSDPP---------------TLNGITFSIPEGALVA 675

Qy    593 ICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEE 652
          : | || || ||:||:| :|  :|| :|| |: ||| ||||| | :||:||||| : :|
Db    676 VVGQVGCGKLSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEP 735

Qy    653 RYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPL 712
            | ||: :| | ||| |||| | ||||||:| ||||||:||:|||||:||:  ||: ||||
Db    736 YYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDDPL 795

Qy    713 SALDAHVGNHIFNSAI--RKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEEL 770
          ||:|||||  ||| : |  :  ||:|| : ||| : ||   | :| |  | |:| |:::||
Db    796 SAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQEL 855

Qy    771 MNLNGDYATIF------------------------------NNLLL----GETPPVEIN 795
          :  :| :|                                  | :|:    |:    :::
Db    856 LARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEAKQMENGMLVTDSAGKQLQRQLS 915

Qy    796 SKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGG 855
          |    ||   :  :    | ::| :| | |  :|:: ::   | |  |||  |::| |
Db    916 SSSSYSGDISRHHN---STAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGL 972

Qy    856 PLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYA 915
          ::|| |  ||| |  |   | :||| |       | |       | |  |:     :
Db    973 FISFLSIF-LFMCNHVSALASNYWLSLWTDDPIVNGT---QEHTKVRLSVYGALGISQGI 1028

Qy    916 SIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRF 975
          :::  |||| :            | : ||  || :|  ||||| ||: ||:| ::|||
Db   1029 AVFGYSMAVSI-----------GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRF 1076

Qy    976 SKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVL 1035
          ||::| ||  :|   :||: ::  |     :|    |   : : || :::     | |
Db   1077 SKELDTVDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIY---FFVQRFY 1133

Qy   1036 I---RELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
          :   |:||||:::::||  ||   :: |:: | |: : : |:|:    :|:|| ::
Db   1134 VASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSI 1193

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
           | |||||||: :   ::    |  |:    :     ||::||::|:|    : ||::||
Db   1194 VANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSE 1253
```

```
Qy    1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
Db    1254 METNIVAVERLKEYSET-EKEAPWQIQETRPPSSWPQVGRVEFRNYCLRYREDLDFVLRH 1312

Qy    1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
Db    1313 INVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITI 1372

Qy    1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
Db    1373 IPQDPVLFSGSLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSV 1432

Qy    1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
Db    1433 GQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIM 1492

Qy    1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAM 1425
Db    1493 DYTRVIVLDKGEIQEYGAPSDLL-QQRGLFYSM 1524
```

Search completed: August 11, 2002, 11:08:49
Job time: 6524 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 11, 2002, 09:20:50 ; Search time 183.28 Seconds
(without alignments)
2759.690 Million cell updates/sec

Title: US-09-528-031-2
Perfect score: 7308
Sequence: 1 MKDIDIGKEYIIPSPGYRSV.....DSSRFYAMFAAAENKVAVKG 1437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7308	100.0	1437	19	US-09-528-031-2	Sequence 2, Appli
2	7298	99.9	1453	12	US-08-843-459-2	Sequence 2, Appli
3	7297	99.8	1437	20	US-09-668-628-19	Sequence 19, Appl
4	7297	99.8	1437	23	US-09-934-421A-6	Sequence 6, Appli
5	7293	99.8	1437	1	PCT-US99-06644-4	Sequence 4, Appli
6	4116	56.3	921	21	US-09-760-470-63	Sequence 63, Appl
7	3037	41.6	1363	21	US-09-775-685-44	Sequence 44, Appl
8	3016.5	41.3	1356	24	US-10-090-280-33	Sequence 33, Appl
9	3015	41.3	1359	24	US-10-090-280-34	Sequence 34, Appl
10	2916.5	39.9	1332	21	US-09-775-685-50	Sequence 50, Appl
11	2865	39.2	569	21	US-09-760-470-51	Sequence 51, Appl
12	2865	39.2	569	21	US-09-760-483-464	Sequence 464, App
13	2643.5	36.2	1331	20	US-09-668-628-1	Sequence 1, Appli
14	2637	36.1	1379	21	US-09-703-253-18	Sequence 18, Appl
15	2583.5	35.4	1216	21	US-09-775-685-46	Sequence 46, Appl
16	2565.5	35.1	1247	21	US-09-775-685-48	Sequence 48, Appl
17	2540.5	34.8	1360	23	US-09-934-421A-2	Sequence 2, Appli
18	2425	33.2	1077	26	US-60-299-484-36	Sequence 36, Appl
19	2401	32.9	1238	26	US-60-207-583-359	Sequence 359, App
20	2316.5	31.7	1216	21	US-09-703-253-24	Sequence 24, Appl
21	2290	31.3	1063	21	US-09-703-253-6	Sequence 6, Appli
22	2086	28.5	1545	26	US-60-333-700-44	Sequence 44, Appl
23	2085	28.5	1545	26	US-60-333-700-4	Sequence 4, Appli
24	2085	28.5	1545	26	US-60-333-700-24	Sequence 24, Appl
25	2085	28.5	1545	26	US-60-333-700-26	Sequence 26, Appl
26	2085	28.5	1545	26	US-60-333-700-28	Sequence 28, Appl
27	2085	28.5	1545	26	US-60-333-700-30	Sequence 30, Appl
28	2085	28.5	1545	26	US-60-333-700-32	Sequence 32, Appl
29	2085	28.5	1545	26	US-60-333-700-34	Sequence 34, Appl
30	2085	28.5	1545	26	US-60-333-700-40	Sequence 40, Appl
31	2085	28.5	1545	26	US-60-333-700-42	Sequence 42, Appl
32	2085	28.5	1545	26	US-60-333-700-46	Sequence 46, Appl
33	2085	28.5	1545	26	US-60-333-700-48	Sequence 48, Appl
34	2084	28.5	1545	26	US-60-333-700-38	Sequence 38, Appl
35	2082	28.5	1531	8	US-08-460-907A-4	Sequence 4, Appli
36	2082	28.5	1531	8	US-08-461-384A-4	Sequence 4, Appli
37	2082	28.5	1531	8	US-08-461-446A-4	Sequence 4, Appli
38	2082	28.5	1531	8	US-08-461-446B-4	Sequence 4, Appli
39	2082	28.5	1531	8	US-08-461-446C-4	Sequence 4, Appli
40	2082	28.5	1531	8	US-08-463-078A-4	Sequence 4, Appli
41	2082	28.5	1531	8	US-08-463-092A-4	Sequence 4, Appli
42	2082	28.5	1545	26	US-60-333-700-36	Sequence 36, Appl
43	2075	28.4	1531	6	US-08-292-309-8	Sequence 8, Appli
44	2075	28.4	1531	8	US-08-407-207-2	Sequence 2, Appli
45	2075	28.4	1531	8	US-08-460-907A-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-528-031-2
; Sequence 2, Application US/09528031
;  GENERAL INFORMATION:
;       APPLICANT: SHYJAN, Andrew
;       TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;                           POLYPEPTIDE
;       NUMBER OF SEQUENCES: 8
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: LAHIVE & COCKFIELD, LLP
;            STREET: 28 State Street
;            CITY: Boston
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/528,031
;            FILING DATE: 17-Mar-2001
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Elizabeth A. Hanley
;            REGISTRATION NUMBER: 33,505
;            REFERENCE/DOCKET NUMBER: MNI-056CP
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617) 227-7400
```

```
;           TELEFAX: (617) 742-4214
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1437 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-528-031-2

  Query Match           100.0%;  Score 7308;  DB 19;  Length 1437;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 1437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Db       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
Db      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Db     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Db     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
Db     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Db     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Db     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
Db     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Db     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Db     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Db     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
Db     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840

Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
Db     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
Db     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
Db     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
Db    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
Db    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
Db    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
Db    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
Db    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
Db    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
Db    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437


RESULT   2
US-08-843-459-2
; Sequence 2, Application US/08843459
;  GENERAL INFORMATION:
;    APPLICANT:  SHYJAN, Andrew
;    TITLE OF INVENTION:  NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
;    TITLE OF INVENTION:  POLYPEPTIDE
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/843,459
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FENTON, Gillian M
;      REGISTRATION NUMBER:  36,508
;      REFERENCE/DOCKET NUMBER:  MIL-001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1453 amino acids
```

```
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-843-459-2


  Query Match             99.9%;  Score 7298;  DB 12;  Length 1453;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1436;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 76

Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      77 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 136

Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     137 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 196

Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 256

Qy     241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 316

Qy     301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 376

Qy     361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 436

Qy     421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 496

Qy     481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 556

Qy     541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 616

Qy     601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 676

Qy     661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     677 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 736

Qy     721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 796

Qy     781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     797 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 856

Qy     841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 916

Qy     901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 976

Qy     961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     977 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1036

Qy    1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1037 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1096

Qy    1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1097 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1156

Qy    1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1157 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1216

Qy    1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1217 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1276

Qy    1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1277 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1336

Qy    1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1337 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1396

Qy    1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1397 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1453


RESULT   3
US-09-668-628-19
; Sequence 19, Application US/09668628
; GENERAL INFORMATION:
;  APPLICANT:  Krasnow, Randi E.
;  APPLICANT:  Baughn, Mariah R.
;  TITLE OF INVENTION:  ATP-BINDING CASSETTE PROTEIN
;  FILE REFERENCE:  PC-0021 US
;  CURRENT APPLICATION NUMBER: US/09/668,628
;  CURRENT FILING DATE:  2000-09-22
;  NUMBER OF SEQ ID NOS:  19
;  SOFTWARE:  PERL Program
; SEQ ID NO 19
;   LENGTH: 1437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: g5685864
US-09-668-628-19


  Query Match             99.8%;  Score 7297;  DB 20;  Length 1437;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1435;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy     181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
```

```
Db    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
Db    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Db    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Db    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
Db    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Db    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Db    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Db    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
Db    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840

Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
Db    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
Db    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
Db    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
Db   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
Db   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
Db   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
Db   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
Db   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
Db   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
Db   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
```

RESULT 4
US-09-934-421A-6
; Sequence 6, Application US/09934421A
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 44589, A NOVEL HUMAN ABC TRANSPORTER
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-083001
; CURRENT APPLICATION NUMBER: US/09/934,421A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/226,770
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-421A-6

Query Match 99.8%; Score 7297; DB 23; Length 1437;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1435; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Db      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
Db     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Db    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Db    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
Db    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Db    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Db    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
```

```
Db    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Db    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Db    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Db    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
Db    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840

Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
Db    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
Db    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
Db    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
Db   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
Db   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
Db   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
Db   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
Db   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
Db   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
Db   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437


RESULT   5
PCT-US99-06644-4
; Sequence 4, Application PC/TUS9906644
; GENERAL INFORMATION:
;  APPLICANT: Fox Chase Cancer Center
;  APPLICANT: Kruh, Gary D.
;  APPLICANT: Lee, Kun
;  APPLICANT: Belinsky, Martin G.
;  APPLICANT: Bain, Lisa J.
;  TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
;  TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
;  FILE REFERENCE: FCCC 98-02
;  CURRENT APPLICATION NUMBER: PCT/US99/06644
;  CURRENT FILING DATE: 1999-03-26
;  EARLIER APPLICATION NUMBER: 60/079,759
;  EARLIER FILING DATE: 1998-03-27
;  EARLIER APPLICATION NUMBER: 60/095,153
;  EARLIER FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 1437
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US99-06644-4


  Query Match             99.8%;  Score 7293;  DB 1;  Length 1437;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1434;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60
Db      1 MKDIDIGKEYIIPSPGYRSVRERTSTSGTHRDREDSKFRRTRPLECQDALETAARAEGLS 60

Qy     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLAR 120
Db     61 LDASMHSQLRILDEEHPKGKYHHGLSALKPIRTTSKHQHPVDNAGLFSCMTFSWLSSLAR 120

Qy    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180
Db    121 VAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLI 180

Qy    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240
Db    181 LSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTW 240

Qy    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300
Db    241 ALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGG 300

Qy    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360
Db    301 PVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNE 360

Qy    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSV 420
Db    361 VLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYFQGITVGVAPIVVVIASVVTFSV 420

Qy    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480
Db    421 HMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIK 480

Qy    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540
Db    481 NKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQA 540

Qy    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600
Db    541 VLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSG 600

Qy    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660
Db    601 KTSLISAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNS 660

Qy    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720
Db    661 CCLRPDLAILPSSDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVG 720

Qy    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780
Db    721 NHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATI 780

Qy    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGS 840
Db    781 FNNLLLGETPPVEINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGS 840
```

```
Qy    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 VPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETS 900

Qy    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 VSDSMKDNPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPM 960

Qy    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 KFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGP 1020

Qy   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 LVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQEL 1080

Qy   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 LDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLT 1140

Qy   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEM 1200

Qy   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 RYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISD 1260

Qy   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 IGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLE 1320

Qy   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 SEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCT 1380

Qy   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 MLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437


RESULT   6
US-09-760-470-63
; Sequence 63, Application US/09760470
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ39
;  CURRENT APPLICATION NUMBER: US/09/760,470
;  CURRENT FILING DATE:  2001-01-16
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 921
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-760-470-63


  Query Match             56.3%;  Score 4116;  DB 21;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  807;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    613 TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPS 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPS 64

Qy    673 SDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHL 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 SDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHL 124

Qy    733 KSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNLLLGETPPV 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 KSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNLLLGETPPV 184

Qy    793 EINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQA 852
          |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db    185 EINSKKETSGSQKKSQDKGPKTGSVKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQA 244

Qy    853 AGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQ 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQ 304

Qy    913 YYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRIL 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 YYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRIL 364

Qy    973 NRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVS 1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 NRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVS 424

Qy   1033 RVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 RVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFT 484

Qy   1093 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 CAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASE 544

Qy   1153 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 TEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKK 604

Qy   1213 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 VSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSI 664

Qy   1273 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 IPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSV 724

Qy   1333 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 GERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVL 784

Qy   1393 GSDRIMVLAQGQVVEFDTPSVLLSNDSS 1420
          ||||||||||||||||||||||||||||
Db    785 GSDRIMVLAQGQVVEFDTPSVLLSNDSS 812


RESULT   7
US-09-775-685-44
; Sequence 44, Application US/09775685
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Wang, Xioming
;  APPLICANT:  Abuin, Alejandro
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Hilbun, Erin
;  TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0128-USA
;  CURRENT APPLICATION NUMBER: US/09/775,685
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,973
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 60/182,422
;  PRIOR FILING DATE: 2000-02-14
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 44
;   LENGTH: 1363
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1363)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-775-685-44
```

Query Match 41.6%; Score 3037; DB 21; Length 1363;
Best Local Similarity 45.3%; Pred. No. 2e-273;
Matches 621; Conservative 254; Mismatches 441; Indels 56; Gaps 14;

```
Qy      80 KYHHGLSALKPIRTTCK-HQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSK 138
           :|   |  : |:|   :   :|||:||| |  |||||: :    :::  |::: :  ||
Db      24 RYDPSLKTMIPVRPCARLAPNPVDDAGLLSFATFSWLTPVMVKGYRQ-RLTVDTLPPLST 82

Qy     139 HESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPA 198
           ::||| | :|   || ||:  |||: |||  ||| | |||::: ||  ::  :    ||
Db      83 YDSSDTNAKRFRVLWDEEVARVGPEKASLSHVVWKFQRTRVLMDIVANILCIIMAAIGPT 142

Qy     199 FMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTMA 258
             ::  :|: |: |   :   : | : |  ||  : :  || ||:|||| :||: |: |:
Db     143 VLIHQILQQTERTSGKVWVGIGLCIALFATEFTKVFFWALAWAINYRTAIRLKVALSTLV 202

Qy     259 FKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPT 318
           |: ::  | :   |:||::|| |:|   :||||    | |  |:: :    |   |||||
Db     203 FENLVSFKTLTHISVGEVLNILSSDSYSLFEAALFCPLPATIPILMVFCAAYAFFILGPT 262

Qy     319 GFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFS 378
             :| :|:::| |  || ::| : |||  :  ||:||| ||| || |: ||||| |:|:
Db     263 ALIGISVYVIFIPVQMFMAKLNSAFRRSAILVTDKRVQTMNEFLTCIRLIKMYAWEKSFT 322

Qy     379 QSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTVVT 438
           ::| ||  ||::|||||: ||    :||||  || |:| | |: |   |||  ||:|:
Db     323 NTIQDIRRRERKLLEKAGFVQSGNSALAPIVSTIAIVLTLSCHILLRRKLTAPVAFSVIA 382

Qy     439 VFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNATLA 498
           :|| | |:: : |||:|:::||:|:: | | : : :       :|  |   : : ||||
Db     383 MFNVMKFSIAILPFSIKAMAEANVSLRRMKKILIDKSPPSYITQPEDPDTVLLLANATLT 442

Qy     499 WDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERPS 558
           |:      : | | |||  ::::    ||::          |  ||
Db     443 WEH-----EASRKSTPKKLQNQKRHLCKKQRSEAYSERSPPA-----KG--------ATG 484

Qy     559 PEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGS 618
           |||:           |:  ||||   :::||::||||:|||||:||::|:|||| | :|
Db     485 PEEQSDS--------LKSVLHSISFVVRKGKILGICGNVGSGKSSLLAALLGQMQLQKGV 536

Qy     619 IAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEI 678
           :|::|| |||:|||||  :  :|:|||||::|| :||   :  | |: ||: ||  |||||
Db     537 VAVNGTLAYVSQQAWIFHGNVRENILFGEKYDHQRYQHTVRVCGLQKDLSNLPYGDLTEI 596

Qy     679 GERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHLKSKTVL 738
           |||| ||||||||||||||:|||| :|:|||||||:|||| |:|   |:| |: |||:
Db     597 GERGLNLSGGQRQRISLARAVYSDRQLYLLDDPLSAVDAHVGKHVFEECIKKTLRGKTVV 656

Qy     739 FVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNL--LLGETP------ 790
           |||||||:|  |||||  :::| | |:|||:|||   | || : :||  |  : |
Db     657 LVTHQLQFLESCDEVILLEDGEICEKGTHKELMEERGRYAKLIHNLRGLQFKDPEHLYNA 716

Qy     791 ---------PVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSV 841
                    | |       :  :| : |  :|||  :    |  | ||:| |   :|:|
Db     717 AMVEAFKESPAEREEDAVLAPGNEKDEGKESETGS--EFVDTKVPEHQLIQTESPQEGTV 774

Qy     842 PWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNET-- 899
           |  |  ||:|:|| |  |  : ||:| :|| ||| |||  |: :||  |   :|| |
Db     775 TWKTYHTYIKASGGYLLSLFTVFLFLLMIGSAAFSNWWLGLWLDKGSRMTCGPQGNRTMC 834

Qy     900 SVSDSMKD-NPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRS 958
           |   : |   |:  |  :|  ||  ||:    :| || | || ||| ||| :| :||:|
```

```
Db     835 EVGAVLADIGQHV--YQWVYTASMVFMLVFGVTKGFVFTKTTLMASSSLHDTVFDKILKS 892

Qy     959 PMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAV 1018
           || ||||||||::||||||||:|||||| || |:|   :| | : ::| |||  |: |
Db     893 PMSFFDTTPTGRLMNRFSKDMDELDVRLPFHAENFLQQFFMVVFILVILAAVFPAVLLVV 952

Qy    1019 GPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQ 1078
             | : | :|  :    ::|||:::|:::||: :|||||:|||  |||| | :  :
Db     953 ASLAVGFFILLRIFHRGVQELKKVENVSRSPWFTHITSSMQGLGIIHAYGKKESCI---T 1009

Qy    1079 ELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQ 1138
           | |:| :    | ||:|| |:|:|::   |  |  |:: |    |  :  ||::|| :|
Db    1010 TLNDENSSHLLYFNCALRWFALRMDVLMNILTFTVALLVTLSFSSISTSSKGLSLSYIIQ 1069

Qy    1139 LTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENA 1198
           |:|| |  ||  :||:|:|||||  :  || |   |    :|      |||  ||:|| :
Db    1070 LSGLLQVCVRTGTETQAKFTSVELLREYISTCVPECTHPLKVGTCPKDWPSXGEITFRDY 1129

Qy    1199 EMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRI 1258
           :||||:| ||||  ::  |:  : :|||||||||||||||||||||| : | | || | |
Db    1130 QMRYRDNTPLVLDSLNLNIQSGQTVGIVGRTGSGKSSLGMALFRLVEPASGTIFIDEVDI 1189

Qy    1259 SDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLK 1318
           : | |||:||::|||:|||| |||| |||||  :|:: :|  |||| |:: | :|| |
Db    1190 CILSLEDLRTKLTVIPQDPVLFVGTVRYNLDPFESHTDEMLWQVLERTFMRDTIMKLPEK 1249

Qy    1319 LESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFAD 1378
           |::|| |||:||||||||||:|||||: ||::|||||:||::|| |:| ||::||
Db    1250 LQAEVTENGENFSVGERQLLCVARALLRNSKIILLDEATASMDSKTDTLVQNTIKDAFKG 1309

Qy    1379 CTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAE 1430
           ||:|||||:|||  | ::|:  |:|:||| | ||     | | ||  |||
Db    1310 CTVLTIAHRLNTVLNCDHVLVMENGKVIEFDKPEVLAEKPDSAF-AMLLAAE 1360
```

```
RESULT   8
US-10-090-280-33
; Sequence 33, Application US/10090280
; GENERAL INFORMATION:
;  APPLICANT: AVENTIS PHARMA SA
;  APPLICANT:  THE GOVERNMENT OF THE UNITED STATES,
;  TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS
;  TITLE OF INVENTION:  CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
;  FILE REFERENCE: ABCC12 GENE
;  CURRENT APPLICATION NUMBER: US/10/090,280
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 60/272,759
;  PRIOR FILING DATE: 2001-03-05
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 1356
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-090-280-33
```

Query Match 41.3%; Score 3016.5; DB 24; Length 1356;
Best Local Similarity 45.0%; Pred. No. 1.6e-271;
Matches 618; Conservative 253; Mismatches 438; Indels 63; Gaps 14;

```
Qy      80 KYHHGLSALKPIRTTCK-HQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSK 138
           :|   |  : |:|   :   :|||:||| |  |||||: :    :::  |::: :  ||
Db      24 RYDPSLKTMIPVRPCARLAPNPVDDAGLLSFATFSWLTPVMVKGYRQ-RLTVDTLPPLST 82

Qy     139 HESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPA 198
           ::||| | :|   || ||:  |||: |||  ||| | |||::: ||  ::  :    ||
Db      83 YDSSDTNAKRFRVLWDEEVARVGPEKASLSHVVWKFQRTRVLMDIVANILCIIMAAIGPT 142

Qy     199 FMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTMA 258
             ::  :|: |: |   :   : | : |  ||  : :  || ||:|||| :||: |: |:
Db     143 VLIHQILQQTERTSGKVWVGIGLCIALFATEFTKVFFWALAWAINYRTAIRLKVALSTLV 202
```

```
Qy    259 FKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPT 318
Db    203 FENLVSFKTLTHISVGEVLNILSSDSYSLFEAALFCPLPATIPILMVFCAAYAFFILGPT 262

Qy    319 GFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFS 378
Db    263 ALIGISVYVIFIPVQMFMAKLNSAFRRSAILVTDKRVQTMNEFLTCIRLIKMYAWEKSFT 322

Qy    379 QSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTVVT 438
Db    323 NTIQDIRRRERKLLEKAGFVQSGNSALAPIVSTIAIVLTLSCHILLRRKLTAPVAFSVIA 382

Qy    439 VFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNATLA 498
Db    383 MFNVMKFSIAILPFSIKAMAEANVSLRRMKKILIDKSPPSYITQPEDPDTVLLLANATLT 442

Qy    499 WDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERPS 558
Db    443 WEH-----EASRKSTPKKLQNQKRHLCKKQRSEAYSERSPPA-----KG--------ATG 484

Qy    559 PEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGS 618
Db    485 PEEQSDS--------LKSVLHSISFVVRKGKILGICGNVGSGKSSLLAALLGQMQLQKGV 536

Qy    619 IAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEI 678
Db    537 VAVNGTLAYVSQQAWIFHGNVRENILFGEKYDHQRYQHTVRVCGLQKDLSNLPYGDLTEI 596

Qy    679 GERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHLKSKTVL 738
Db    597 GERGLNLSGGQRQRISLARAVYSDRQLYLLDDPLSAVDAHVGKHVFEECIKKTLRGKTVV 656

Qy    739 FVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNL--LLGETP------ 790
Db    657 LVTHQLQFLESCDEVILLEDGEICEKGTHKELMEERGRYAKLIHNLRGLQFKDPEHLYNA 716

Qy    791 ---------PVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSV 841
Db    717 AMVEAFKESPAEREEDAVLAPGNEKDEGKESETGS--EFVDTKVPEHQLIQTESPQEGTV 774

Qy    842 PWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNET-- 899
Db    775 TWKTYHTYIKASGGYLLSLFTVFLFLLMIGSAAFSNWWLGLWLDKGSRMTCGPQGNRTMC 834

Qy    900 SVSDSMKD-NPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRS 958
Db    835 EVGAVLADIGQHV--YQWVYTASMVFMLVFGVTKGFVFTKTTLMASSSLHDTVFDKILKS 892

Qy    959 PMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAV 1018
Db    893 PMSFFDTTPTGRLMNRFSKDMDELDVRLPFHAENFLQQFFMVVFILVILAAVFPAVLLVV 952

Qy   1019 GPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQ 1078
Db    953 ASLAVGFFILLRIFHRGVQELKKVENVSRSPWFTHITSSMQGLGIIHAYGKKESCITYH- 1011

Qy   1079 ELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQ 1138
Db   1012 ---------LLYFNCALRWFALRMDVLMNILTFTVALLVTLSFSSISTSSKGLSLSYIIQ 1062

Qy   1139 LTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENA 1198
Db   1063 LSGLLQVCVRTGTETQAKFTSVELLREYISTCVPECTHPLKVGTCPKDWPSCGEITFRDY 1122

Qy   1199 EMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRI 1258
Db   1123 QMRYRDNTPLVLDSLNLNIQSGQTVGIVGRTGSGKSSLGMALFRLVEPASGTIFIDEVDI 1182

Qy   1259 SDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLK 1318
Db   1183 CILSLEDLRTKLTVIPQDPVLFVGTVRYNLDPFESHTDEMLWQVLERTFMRDTIMKLPEK 1242

Qy   1319 LESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFAD 1378
```

```
Db   1243 LQAEVTENGENFSVGERQLLCVARALLRNSKIILLDEATASMDSKTDTLVQNTIKDAFKG 1302

Qy   1379 CTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAE 1430
Db   1303 CTVLTIAHRLNTVLNCDHVLVMENGKVIEFDKPEVLAEKPDSAF-AMLLAAE 1353


RESULT   9
US-10-090-280-34
; Sequence 34, Application US/10090280
; GENERAL INFORMATION:
;  APPLICANT: AVENTIS PHARMA SA
;  APPLICANT:  THE GOVERNMENT OF THE UNITED STATES,
;  TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS
;  TITLE OF INVENTION:  CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
;  FILE REFERENCE: ABCC12 GENE
;  CURRENT APPLICATION NUMBER: US/10/090,280
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: 60/272,759
;  PRIOR FILING DATE: 2001-03-05
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 1359
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-090-280-34


  Query Match             41.3%;  Score 3015;  DB 24;  Length 1359;
  Best Local Similarity   44.8%;  Pred. No. 2.3e-271;
  Matches  618;  Conservative  255;  Mismatches  432;  Indels   74;  Gaps   15;

Qy      80 KYHHGLSALKPIRTTCK-HQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSK 138
Db      24 RYDPSLKTMIPVRPCARLAPNPVDDAGLLSFATFSWLTPVMVKGYRQ-RLTVDTLPPLST 82

Qy     139 HESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPA 198
Db      83 YDSSDTNAKRFRVLWDEEVARVGPEKASLSHVVWKFQRTRVLMDIVANILCIIMAAIGPT 142

Qy     199 FMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTMA 258
Db     143 VLIHQILQQTERTSGKVWVGIGLCIALFATEFTKVFFWALAWAINYRTAIRLKVALSTLV 202

Qy     259 FKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPT 318
Db     203 FENLVSFKTLTHISVGEVLNILSSDSYSLFEAALFCPLPATIPILMVFCAAYAFFILGPT 262

Qy     319 GFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFS 378
Db     263 ALIGISVYVIFIPVQMFMAKLNSAFRRSAILVTDKRVQTMNEFLTCIRLIKMYAWEKSFT 322

Qy     379 QSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTVVT 438
Db     323 NTIQDIRRRERKLLEKAGFVQSGNSALAPIVSTIAIVLTLSCHILLRRKLTAPVAFSVIA 382

Qy     439 VFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNATLA 498
Db     383 MFNVMKFSIAILPFSIKAMAEANVSLRRMKKILIDKSPPSYITQPEDPDTVLLLANATLT 442

Qy     499 WDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERPS 558
Db     443 WEH-----EASRKSTPKKLQNQKRHLCKKQRSEAYSERSPPA-----KG--------ATG 484

Qy     559 PEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGS 618
Db     485 PEEQSDS--------LKSVLHSISFVVRKGKILGICGNVGSGKSSLLAALLGQMQLQKGV 536

Qy     619 IAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEI 678
Db     537 VAVNGTLAYVSQQAWIFHGNVRENILFGEKYDHQRYQHTVRVCGLQKDLSNLPYGDLTEI 596
```

```
Qy    679 GERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHLKSKTVL 738
          |||||  |||||||||||||||||:||||  :|:|||||||:|||||  |:|    |:|  |: |||:
Db    597 GERGLNLSGGQRQRISLARAVYSDRQLYLLDDPLSAVDAHVGKHVFEECIKKTLRGKTVV 656

Qy    739 FVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNL-------------- 784
          |||||||:|  |||||  :::| | |:|||:|||   | || : :||
Db    657 LVTHQLQFLESCDEVILLEDGEICEKGTHKELMEERGRYAKLIHNLRGLQFKDPEHLYNA 716

Qy    785 ----LLGETPPVEINSKKETSG------SQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLE 834
              |:|      ::| :|        :| : |  :||| :    |  | ||:| |
Db    717 AMVEAFKESPA----EREEDAGIIVLAPGNEKDEGKESETGS--EFVDTKVPEHQLIQTE 770

Qy    835 EKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVT 894
            :|:| |  |  ||:|:|| |  |  : ||:| :|| ||| |||  |: :||  |
Db    771 SPQEGTVTWKTYHTYIKASGGYLLSLFTVFLFLLMIGSAAFSNWWLGLWLDKGSRMTCGP 830

Qy    895 RGNET--SVSDSMKD-NPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDEL 951
          :|| |   |   : |   |:  |  :|  ||  ||:    :| || | || ||| ||| :
Db    831 QGNRTMCEVGAVLADIGQHV--YQWVYTASMVFMLVFGVTKGFVFTKTTLMASSSLHDTV 888

Qy    952 FRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVF 1011
          | :||:||| |||||||||::|||||||||:|||||| || |:|   :| | : ::| ||
Db    889 FDKILKSPMSFFDTTPTGRLMNRFSKDMDELDVRLPFHAENFLQQFFMVVFILVILAAVF 948

Qy   1012 PWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQ 1071
          |  |: |  | : | :|  :    ::|||:::|:::||: :|||||:|||  |||| | :
Db    949 PAVLLVVASLAVGFFILLRIFHRGVQELKKVENVSRSPWFTHITSSMQGLGIIHAYGKKE 1008

Qy   1072 EFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGL 1131
            :  :             | ||:|| |:|:|::   |  |  |::|    |  :  ||
Db   1009 SCITYH----------LLYFNCALRWFALRMDVLMNILTFTVALLVTLSFSSISTSSKGL 1058

Qy   1132 AISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEG 1191
          ::|| :||:|| |  ||  :||:|:|||| :  || |   |    :|      |||  |
Db   1059 SLSYIIQLSGLLQVCVRTGTETQAKFTSVELLREYISTCVPECTHPLKVGTCPKDWPSCG 1118

Qy   1192 EVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCI 1251
          |:|| : :||||:| ||||  ::  |:  : :|||||||||||||||||||||| : | |
Db   1119 EITFRDYQMRYRDNTPLVLDSLNLNIQSGQTVGIVGRTGSGKSSLGMALFRLVEPASGTI 1178

Qy   1252 KIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKEC 1311
            || | |  : | |||:||::|||:|||| |||| |||||  :|:: :|  ||||  |::
Db   1179 FIDEVDICILSLEDLRTKLTVIPQDPVLFVGTVRYNLDPFESHTDEMLWQVLERTFMRDT 1238

Qy   1312 IAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQET 1371
          | :|| ||::|| |||:|||||||||||:|||||: ||::|||||:||::|| |:| |
Db   1239 IMKLPEKLQAEVTENGENFSVGERQLLCVARALLRNSKIILLDEATASMDSKTDTLVQNT 1298

Qy   1372 IREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAE 1430
          |::||  ||:|||||||:|||  | ::|:  |:|:||| | ||    | | ||  |||
Db   1299 IKDAFKGCTVLTIAHRLNTVLNCDHVLVMENGKVIEFDKPEVLAEKPDSAF-AMLLAAE 1356


RESULT 10
US-09-775-685-50
; Sequence 50, Application US/09775685
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Wang, Xioming
;  APPLICANT:  Abuin, Alejandro
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Hilbun, Erin
;  TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding the
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0128-USA
;  CURRENT APPLICATION NUMBER: US/09/775,685
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,973
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 60/182,422
;  PRIOR FILING DATE: 2000-02-14
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 1332
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1332)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-775-685-50


  Query Match             39.9%;  Score 2916.5;  DB 21;  Length 1332;
  Best Local Similarity   44.1%;  Pred. No. 3.7e-262;
  Matches  605;  Conservative  248;  Mismatches  432;  Indels   87;  Gaps   15;

Qy     80 KYHHGLSALKPIRTTCK-HQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSK 138
          :|   |  : |:|   :   :|||:||| |  |||||: :    :::  |::: :  ||
Db     24 RYDPSLKTMIPVRPCARLAPNPVDDAGLLSFATFSWLTPVMVKGYRQ-RLTVDTLPPLST 82

Qy    139 HESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPA 198
          ::||| | :|   || ||:  |||: |||  ||| | |||::: ||  ::  :    ||
Db     83 YDSSDTNAKRFRVLWDEEVARVGPEKASLSHVVWKFQRTRVLMDIVANILCIIMAAIGPT 142

Qy    199 FMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTMA 258
          ::  :|: |: |   :  | : |  ||  : :  || ||:|||| :||: |: |:
Db    143 VLIHQILQQTERTSGKVWVGIGLCIALFATEFTKVFFWALAWAINYRTAIRLKVALSTLV 202

Qy    259 FKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPT 318
          |: ::  | :   |:||::|| |:|   :|||     | |  |:: :    |  |||||
Db    203 FENLVSFKTLTHISVGEVLNILSSDSYSLFEAALFCPLPATIPILMVFCAAYAFFILGPT 262

Qy    319 GFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFS 378
            :| :|:::| |  || ::| : |||  :  ||:||| ||| || |: |||||  |:|:
Db    263 ALIGISVYVIFIPVQMFMAKLNSAFRRSAILVTDKRVQTMNEFLTCIRLIKMYAWEKSFT 322

Qy    379 QSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTVVT 438
          ::| ||  ||::|||||: ||    :||||  || |:| | |: |   |||  ||:|:
Db    323 NTIQDIRRRERKLLEKAGFVQSGNSALAPIVSTIAIVLTLSCHILLRRKLTAPVAFSVIA 382

Qy    439 VFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNATLA 498
          :|| | |:: : |||:|:::||:|:: | | : : :        :|  |   : : ||||
Db    383 MFNVMKFSIAILPFSIKAMAEANVSLRRMKKILIDKSPPSYITQPEDPDTVLLLANATLT 442

Qy    499 WDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERPS 558
          |:      : | | |||  ::::    ||::           |     ||
Db    443 WEH-----EASRKSTPKKLQNQKRHLCKKQRSEAYSERSPPA-----KG--------ATG 484

Qy    559 PEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGS 618
          |||:           |:  ||||   :::||:::||||:|||||:||::|:|||| | :|
Db    485 PEEQSDS--------LKSVLHSISFVVRKGKILGICGNVGSGKSSLLAALLGQMQLQKGV 536

Qy    619 IAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEI 678
          :|::|| |||:||||| :  :|:|||||::|| :||   :  | |: ||: ||  |||||
Db    537 VAVNGTLAYVSQQAWIFHGNVRENILFGEKYDHQRYQHTVRVCGLQKDLSNLPYGDLTEI 596

Qy    679 GERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHLKSKTVL 738
          |||| ||||||||||||||:|||| :|:|||||||:||||  |:|    |:| |: |||:
Db    597 GERGLNLSGGQRQRISLARAVYSDRQLYLLDDPLSAVDAHVGKHVFEECIKKTLRGKTVV 656

Qy    739 FVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNL--LLGETP------ 790
          ||||||:|  |||| :::| | |:|||:|||   | || : :||  |  : |
Db    657 LVTHQLQFLESCDEVILLEDGEICEKGTHKELMEERGRYAKLIHNLRGLQFKDPEHLYNA 716

Qy    791 ---------PVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSV 841
                  | |       :  :| : |  :|||  :    |  | ||:| |   :|:|
Db    717 AMVEAFKESPAEREEDAVLAPGNEKDEGKESETGS--EFVDTKVPEHQLIQTESPQEGTV 774

Qy    842 PWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNET-- 899
```

```
Db    775 TWKTYHTYIKASGGYLLSLFTVFLFLLMIGSAAFSNWWLGLWLDKGSRMTCGPQGNRTMC 834

Qy    900 SVSDSMKD-NPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRS 958
Db    835 EVGAVLADIGQHV--YQWVYTASMVFMLVFGVTKGFVFTKTTLMASSSLHDTVFDKILKS 892

Qy    959 PMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAV 1018
Db    893 PMSFFDTTPTGRLMNRFSKDMDELDVRLPFHAENFLQQFFMVVFILVILAAVFPAVLLVV 952

Qy   1019 GPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQ 1078
Db    953 ASLAVGFFILLRIFHRGVQELKKVENVSRSPWFTHITSSMQGLGIIHAYGKKESCI---T 1009

Qy   1079 ELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQ 1138
Db   1010 TLNDENSSHLLYFNCALRWFALRMDVLMNILTFTVALLVTLSFSSISTSSKGLSLSYIIQ 1069

Qy   1139 LTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENA 1198
Db   1070 LSGLLQVCVRTGTETQAKFTSVELLREYISTCVPECTHPLKVGTCPKDWPSXGEITFRDY 1129

Qy   1199 EMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRI 1258
Db   1130 QMRYRDNTPLVLDSLNLNIQSGQTVGIVGRTGSGKSSLGMALFRLVEPASGTIFIDEVDI 1189

Qy   1259 SDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLK 1318
Db   1190 CILSLEDLRTKLTVIPQDPVLF----------IMKLPEK 1218

Qy   1319 LESEVMENGDNFSVGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFAD 1378
Db   1219 LQAEVTENGENFSVGERQLLCVARALLRNSKIILLDEATASMDSKTDTLVQNTIKDAFKG 1278

Qy   1379 CTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAE 1430
Db   1279 CTVLTIAHRLNTVLNCDHVLVMENGKVIEFDKPEVLAEKPDSAF-AMLLAAE 1329
```

RESULT 11
US-09-760-470-51
; Sequence 51, Application US/09760470
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ39
; CURRENT APPLICATION NUMBER: US/09/760,470
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (243)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (250)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (437)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-470-51

Query Match 39.2%; Score 2865; DB 21; Length 569;

Best Local Similarity 99.1%; Pred. No. 5.2e-258;
Matches 564; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy    869 NVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLIL 928
Db      1 NVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLIL 60

Qy    929 KAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPF 988
Db     61 KAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPF 120

Qy    989 QAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQS 1048
Db    121 QAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQS 180

Qy   1049 PFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIA 1108
Db    181 PFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIA 240

Qy   1109 LITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIK 1168
Db    241 LIXXTGLMIXLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIK 300

Qy   1169 TLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGR 1228
Db    301 TLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGR 360

Qy   1229 TGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNL 1288
Db    361 TGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNL 420

Qy   1289 DPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHC 1348
Db    421 DPFNQYTEDQIWDALEXTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHC 480

Qy   1349 KILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEF 1408
Db    481 KILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRFMVLAQGQVVEF 540

Qy   1409 DTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
Db    541 DTPSVLLSNDSSRFYAMFAAAENKVAVKG 569
```

RESULT 12
US-09-760-483-464
; Sequence 464, Application US/09760483
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ14
; CURRENT APPLICATION NUMBER: US/09/760,483
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 856
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 464
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (243)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (250)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (437)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-760-483-464

Query Match 39.2%; Score 2865; DB 21; Length 569;
Best Local Similarity 99.1%; Pred. No. 5.2e-258;
Matches 564; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy    869 NVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLIL 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 NVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMAVMLIL 60

Qy    929 KAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPF 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 KAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPF 120

Qy    989 QAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQS 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQS 180

Qy   1049 PFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIA 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIA 240

Qy   1109 LITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIK 1168
          ||  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LIXXTGLMIXLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIK 300

Qy   1169 TLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGR 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGR 360

Qy   1229 TGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNL 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNL 420

Qy   1289 DPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHC 1348
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 DPFNQYTEDQIWDALEXTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHC 480

Qy   1349 KILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEF 1408
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    481 KILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRFMVLAQGQVVEF 540

Qy   1409 DTPSVLLSNDSSRFYAMFAAAENKVAVKG 1437
          |||||||||||||||||||||||||||||
Db    541 DTPSVLLSNDSSRFYAMFAAAENKVAVKG 569
```

RESULT 13
US-09-668-628-1
; Sequence 1, Application US/09668628
; GENERAL INFORMATION:
; APPLICANT: Krasnow, Randi E.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: ATP-BINDING CASSETTE PROTEIN
; FILE REFERENCE: PC-0021 US
; CURRENT APPLICATION NUMBER: US/09/668,628
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 1331
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7481813CD1
US-09-668-628-1

Query Match 36.2%; Score 2643.5; DB 20; Length 1331;
Best Local Similarity 40.9%; Pred. No. 1.4e-236;
Matches 548; Conservative 258; Mismatches 487; Indels 47; Gaps 7;

```
Qy     99 HPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSKHESSDVNCRRLERLWQEELN 158
          :|:|||||||| :| |||: |  :   :  |    :  || |::|| | :|| |||:||:: 
Db     33 YPLDNAGLFSYLTVSWLTPL-MIQSLRSRLDENTIPPLSVHDASDKNVQRLHRLWEEEVS 91

Qy    159 EVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPAFMVKHLLEYTQATESNLQYS 218
            | : ||:  |:  | |||||   :  :  :|   ||  ::  :|||::    |: : 
Db     92 RRGIEKASVLLVMLRFQRTRLIFDALLGICFCIASVLGPILIIPKILEYSEEQLGNVVHG 151

Qy    219 LLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTMAFKKILKLKNIKEKSLGELIN 278
          : |   | |:| |:| | : :| :| || :| | |: : ||:|::: |::   : ||:|: 
Db    152 VGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSSFAFEKLIQFKSVIHITSGEVIS 211

Qy    279 ICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPTGFLGSAVFILFYPAMMFASR 338
            : |   :||    | |:       ::  | :  |:| | |:    ::| :|  :| :| 
Db    212 FFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIGYTAFIAILCYLLVFPLAVFMTR 271

Qy    339 LTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFSQSVQKIREEERRILEKAGYF 398
          :    :      :|:|::  :|||| || |||| | | |:: :: :| :||::||| |
Db    272 MAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKPFAKIIEDLRRKERKLLEKCGLV 331

Qy    399 QSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTVVTVFNSMTFALKVTPFSVKSLS 458
          ||:|     |:  :|: |   :| :|   | |: ||:::   | :  ::   | :|| :
Db    332 QSLTSITLFIIPTVATAVWVLIHTSLKLKLAASMAFSMLASLNLLRLSVFFVPIAVKGPT 391

Qy    459 EASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNATLAWDSSHSSIQNSPKLTPKMKK 518
          :  || |||  || |       |   : : |||:|  :   | |
Db    392 NSKSAVMRFKKFFLQESPVFYVQTLQDPSKALVFEEATLSWQQTCPGIVNG--------- 442

Qy    519 DKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERP----SPEEEEGKHIHLGHLRL 574
                                  |:  |: ||   :   ||     ||||          |
Db    443 ----------------------ALELERNGH-ASEGMTRPRDALGPEEEGNS--------L 472

Qy    575 QRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGSIAISGTFAYVAQQAWI 634
            || |:| : :| ::|:||: |||||:||:|||| :| ||||||: : |: ||| |||||
Db    473 GPELHKINLVVSKGMMLGVCGNTGSGKSSLLSAILEEMHLLEGSVGVQGSLAYVPQQAWI 532

Qy    635 LNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEIGERGANLSGGQRQRIS 694
          ::  :|:||| |  ||: ||  ||: | |  || :|| |:|||||| ||||||:||||
Db    533 VSGNIRENILMGGAYDKARYLQVLHCCSLNRDLELLPFGDMTEIGERGLNLSGGQKQRIS 592

Qy    695 LARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHLKSKTVLFVTHQLQYLVDCDEVI 754
          ||||:|||| ||:|||||||:|||||  |||   |:| |: |||: ||||||||  | ::|
Db    593 LARAVYSDRQIYLLDDPLSAVDAHVGKHIFEECIKKTLRGKTVVLVTHQLQYLEFCGQII 652

Qy    755 FMKEGCITERGTHEELMNLNGDYATIFNNLLLGETPPVEINSKKETSGSQKKSQDKGPKT 814
            :: | | | ||| |||   | || :   :    |  :  :: |     : :||
Db    653 LLENGKICENGTHSELMQKKGKYAQLIQKMHKEATSDMLQDTAKIAEKPKVESQALATSL 712

Qy    815 GSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTA 874
                ||   | || | ||  :||: | ||  |||||||  :   :|   :| | |
Db    713 EESLNGNAV--PEHQLTQEEEMEEGSLSWRVYHHYIQAAGGYMVSCIIFFFVVLIVFLTI 770

Qy    875 FSTWWLSYWIKQGSGNTTVTRGNETSVS-DSMKDNPHMQYYASIYALSMAVMLILKAIRG 933
          || ||||||::||||  :    | |      :: ||| : :|  :| |:  ::: :
Db    771 FSFWWLSYWLEQGSGTNSSRESNGTMADLGNIADNPQLSFYQLVYGLNALLLICVGVCSS 830

Qy    934 VVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMF 993
            :| | | :||: ||:::|| :: | || |||| | ||:|| |: |::::|  ||  :| | |
Db    831 GIFTKVTRKASTALHNKLFNKVFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQF 890

Qy    994 IQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSH 1053
          :   ::|   : ::: : |: |:    ::::  : ::: :  |   |||:| ::||  ||
Db    891 LVLSLMVIAVLLIVSVLSPYILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPLFSH 950

Qy   1054 ITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTT 1113
          | :|:|||::|| | | ::|: ::: | |       ||  : ||:|:||:::  :
Db    951 ILNSLQGLSSIHVYGKTEDFISQFKRLTDAQNNYLLLFLSSTRWMALRLEIMTNLVTLAV 1010

Qy   1114 GLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTLSLE 1173
          | :       | ::  :|::  :||   || | |:  ||||:||:|||  |:|    |
Db   1011 ALFVAFGISSTPYSFKVMAVNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSE 1070
```

```
Qy   1174 APARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGK 1233
Db   1071 APLHMEGTSCPQGWPQHGEIIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGK 1130

Qy   1234 SSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLSIIPQEPVLFSGTVRSNLDPFNQ 1293
Db   1131 SSLGMALFRLVEPMAGRILIDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDR 1190

Qy   1294 YTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFSVGERQLLCIARALLRHCKILIL 1353
Db   1191 HTDQQIWDALERTFLTKAISKFPKKLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILI 1250

Qy   1354 DEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTVLGSDRIMVLAQGQVVEFDTPSV 1413
Db   1251 DEATASIDMETDTLIQRTIREAFQGCTVLVIAHRVTTVLNCDRILVMGNGKVVEFDRPEV 1310

Qy   1414 LLSNDSSRFYAMFAAAENKV 1433
Db   1311 LRKKPGSLFAALMATATSSL 1330
```

```
RESULT  14
US-09-703-253-18
; Sequence 18, Application US/09703253
; GENERAL INFORMATION:
;  APPLICANT: Harras, Marie
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Turner, C. Alexander Jr.
;  APPLICANT:  Nehls, Michael
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: Novel Human Transporter Proteins and
;  TITLE OF INVENTION:  Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0081-USA
;  CURRENT APPLICATION NUMBER: US/09/703,253
;  CURRENT FILING DATE:  2000-10-31
;  PRIOR APPLICATION NUMBER: US 60/163,018
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1379
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-703-253-18
```

```
  Query Match           36.1%;  Score 2637;  DB 21;  Length 1379;
  Best Local Similarity  40.5%;  Pred. No. 5.9e-236;
  Matches  552;  Conservative  258;  Mismatches  504;  Indels   48;  Gaps    8;

Qy     77 PKGKYHHGLSALKPIRTTCKHQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSL 136
Db     60 PWGKYDAALRTMIPFRPKPRFPAP-QPLGLFSYLTVSWLTPL-MIQSLRSRLDENTIPPL 117

Qy    137 SKHESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSG 196
Db    118 SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTRLIFDALLGICFCIASVLG 177

Qy    197 PAFMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILT 256
Db    178 PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS 237

Qy    257 MAFKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILG 316
Db    238 FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG 297

Qy    317 PTGFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKA 376
Db    298 YTAFIAILCYLLVFPLEVFMTRMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP 357

Qy    377 FSQSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTV 436
```

```
Db    358 FAKIIEDLRRKERKLLEKCGLVQSLTSITLFIIPTVATAVWVLIHTSLKLKLTASMAFSM 417

Qy    437 VTVFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNAT 496
Db    418 LASLNLLRLSVFFVPIAVKGLTNSKSAVMRFKKFFLQESPVFYVQTLQDPSKALVFEEAT 477

Qy    497 LAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDER 556
Db    478 LSWQQTCPGIVNG----------------------------ALELERNGH-ASEGMTR 506

Qy    557 P----SPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQM 612
Db    507 PRDALGPEEEGNS--------LGPELHKINLVVSKGMMLGVCGNTGSGKSSLLSAILEEM 558

Qy    613 TLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPS 672
Db    559 HLLEGSVGVQGSLAYVPQQAWIVSGNIRENILMGGAYDKARYLQVLHCCSLNRDLELLPF 618

Qy    673 SDLTEIGERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHL 732
Db    619 GDMTEIGERGLNLSGGQKQRISLARAVYSDRQIYLLDDPLSAVDAHVGKHIFEECIKKTL 678

Qy    733 KSKTVLFVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNLLLGETPPV 792
Db    679 RGKTVVLVTHQLQYLEFCGQIILLENGKICENGTHSELMQKKGKYAQLIQKMHKEATSDM 738

Qy    793 EINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSVPWSVYGVYIQA 852
Db    739 LQDTAKIAEKPKVESQALATSLEESLNGNAV--PEHQLTQEEEMEEGSLSWRVYHHYIQA 796

Qy    853 AGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNETSVS-DSMKDNPHM 911
Db    797 AGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQGSGTNSSRESNGTMADLGNIADNPQL 856

Qy    912 QYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRSPMKFFDTTPTGRI 971
Db    857 SFYQLVYGLNALLLICVGVCSSGIFTKVTRKASTALHNKLFNKVFRCPMSFFDTIPIGRL 916

Qy    972 LNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAVGPLVILFSVLHIV 1031
Db    917 LNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSPYILLMGAIIMVICFIYYMM 976

Qy   1032 SRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQELLDDNQAPFFLF 1091
Db    977 FKKAIGVFKRLENYSRSPLFSHILNSLQGLSSIHVYGKTEDFISQFKRLTDAQNNYLLLF 1036

Qy   1092 TCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLAS 1151
Db   1037 LSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMAVNIVLQLASSFQATARIGL 1096

Qy   1152 ETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENAEMRYRENLPLVLK 1211
Db   1097 ETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGEIIFQDYHMKYRDNTPTVLH 1156

Qy   1212 KVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRISDIGLADLRSKLS 1271
Db   1157 GINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRILIDGVDICSIGLEDLRSKLS 1216

Qy   1272 IIPQEPVLFSGTVRSNLDPFNQYTEDQIWDALERTHMKECIAQLPLKLESEVMENGDNFS 1331
Db   1217 VIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKAISKFPKKLHTDVVENGGNFS 1276

Qy   1332 VGERQLLCIARALLRHCKILILDEATAAMDTETDLLIQETIREAFADCTMLTIAHRLHTV 1391
Db   1277 VGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTIREAFQGCTVLVIAHRVTTV 1336

Qy   1392 LGSDRIMVLAQGQVVEFDTPSVLLSNDSSRFYAMFAAAENKV 1433
Db   1337 LNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSSL 1378
```

RESULT 15

```
US-09-775-685-46
; Sequence 46, Application US/09775685
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Wang, Xioming
;  APPLICANT:  Abuin, Alejandro
;  APPLICANT:  Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  APPLICANT:  Donoho, Gregory
;  APPLICANT:  Hilbun, Erin
;  TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding the
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0128-USA
;  CURRENT APPLICATION NUMBER: US/09/775,685
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,973
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 60/182,422
;  PRIOR FILING DATE: 2000-02-14
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 1216
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1216)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-775-685-46
```

Query Match 35.4%; Score 2583.5; DB 21; Length 1216;
Best Local Similarity 43.6%; Pred. No. 4.8e-231;
Matches 535; Conservative 227; Mismatches 410; Indels 55; Gaps 13;

```
Qy      80 KYHHGLSALKPIRTTCK-HQHPVDNAGLFSCMTFSWLSSLARVAHKKGELSMEDVWSLSK 138
           :|    |  : |:|   :   :|||:||| |  |||||: :    ::: |::: :  ||
Db      24 RYDPSLKTMIPVRPCARLAPNPVDDAGLLSFATFSWLTPVMVKGYRQ-RLTVDTLPPLST 82

Qy     139 HESSDVNCRRLERLWQEELNEVGPDAASLRRVVWIFCRTRLILSIVCLMITQLAGFSGPA 198
           ::||| | :|   || ||:  |||: ||| ||| | |||::: ||  ::  :    ||
Db      83 YDSSDTNAKRFRVLWDEEVARVGPEKASLSHVVWKFQRTRVLMDIVANILCIIMAAIGPT 142

Qy     199 FMVKHLLEYTQATESNLQYSLLLVLGLLLTEIVRSWSLALTWALNYRTGVRLRGAILTMA 258
           ::  :|: |: |   :   : | : |  ||  : :  || ||:|||| :||: |: |:
Db     143 VLIHQILQQTERTSGKVWVGIGLCIALFATEFTKVFFWALAWAINYRTAIRLKVALSTLV 202

Qy     259 FKKILKLKNIKEKSLGELINICSNDGQRMFEAAAVGSLLAGGPVVAILGMIYNVIILGPT 318
           |: ::  | :   |:||::|| |:|   :|||| |  |  |:: :   |  |||||
Db     203 FENLVSFKTLTHISVGEVLNILSSDSYSLFEAALFCPLPATIPILMVFCAAYAFFILGPT 262

Qy     319 GFLGSAVFILFYPAMMFASRLTAYFRRKCVAATDERVQKMNEVLTYIKFIKMYAWVKAFS 378
           :| :|:::| |  || ::| : |||  :  ||:||| ||| || |: |||||| |:|:
Db     263 ALIGISVYVIFIPVQMFMAKLNSAFRRSAILVTDKRVQTMNEELTCIRLIKMYAWEKSFT 322

Qy     379 QSVQKIREEERRILEKAGYFQSITVGVAPIVVVIASVVTFSVHMTLGFDLTAAQAFTVVT 438
           ::| ||  ||::|||||: ||    :|||| || |:| | |: |   |||  ||:|:
Db     323 NTIQDIRRRERKLLEKAGFVQSGNSALAPIVSTIAIVLTLSCHILLRRKLTAPVAFSVIA 382

Qy     439 VFNSMTFALKVTPFSVKSLSEASVAVDRFKSLFLMEEVHMIKNKPASPHIKIEMKNATLA 498
           :|| | |:: :.|||:|:::||:|:: | | : : :       :|  |   : : ||||
Db     383 MFNVMKFSIAILPFSIKAMAEANVSLRRMKKILIDKSPPSYITQPEDPDTVLLLANATLT 442

Qy     499 WDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQRTEHQAVLAEQKGHLLLDSDERPS 558
           |:      : | | |||  ::::    ||::          | : ||
Db     443 WEH-----EASRKSTPKKLQNQKRHLCKKQRSEAYSERSPPA-----KG--------ATG 484

Qy     559 PEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGICGSVGSGKTSLISAILGQMTLLEGS 618
           |||:          |:  |||   :::||::||||:|||||:||::|:|||| | :|
Db     485 PEEQSDS--------LKSVLHSISFVVRKGKILGICGNVGSGKSSLLAALLGQMQLQKGV 536

Qy     619 IAISGTFAYVAQQAWILNATLRDNILFGKEYDEERYNSVLNSCCLRPDLAILPSSDLTEI 678
           :|::|| |||:||||| :  :|:||||||::|| :||   :  | |: ||: ||  ||||||
Db     537 VAVNGTLAYVSQQAWIFHGNVRENILFGEKYDHQRYQHTVRVCGLQKDLSNLPYGDLTEI 596

Qy     679 GERGANLSGGQRQRISLARALYSDRSIYILDDPLSALDAHVGNHIFNSAIRKHLKSKTVL 738
           |||| ||||||||||||||||:|||| :|:|||||||:||||| |:|   |:| |: |||:
Db     597 GERGLNLSGGQRQRISLARAVYSDRQLYLLDDPLSAVDAHVGKHVFEECIKKTLRGKTVV 656

Qy     739 FVTHQLQYLVDCDEVIFMKEGCITERGTHEELMNLNGDYATIFNNL--LLGETP------ 790
           ||||||:|  ||||| :::| | |:|||:|||   | || : :||  |  : |
Db     657 LVTHQLQFLESCDEVILLEDGEICEKGTHKELMEERGRYAKLIHNLRGLQFKDPEHLYNA 716

Qy     791 ---------PVEINSKKETSGSQKKSQDKGPKTGSIKKEKAVKPEEGQLVQLEEKGQGSV 841
                    | |       :  :| : |  :|||  :    |  | ||:| |   :|:|
Db     717 AMVEAFKESPAEREEDAVLAPGNEKDEGKESETGS--EFVDTKVPEHQLIQTESPQEGTV 774

Qy     842 PWSVYGVYIQAAGGPLAFLVIMALFMLNVGSTAFSTWWLSYWIKQGSGNTTVTRGNET-- 899
           |  |  ||:|:|| |  |  : ||:| :|| ||| |||  |: :||  |   :|| |
Db     775 TWKTYHTYIKASGGYLLSLFTVFLFLLMIGSAAFSNWWLGLWLDKGSRMTCGPQGNRTMC 834

Qy     900 SVSDSMKD-NPHMQYYASIYALSMAVMLILKAIRGVVFVKGTLRASSRLHDELFRRILRS 958
           |   : |   |:  |  :|  ||  ||:    :| || | || ||| ||| :| :||:|
Db     835 EVGAVLADIGQHV--YQWVYTASMVFMLVFGVTKGFVFTKTTLMASSSLHDTVFDKILKS 892

Qy     959 PMKFFDTTPTGRILNRFSKDMDEVDVRLPFQAEMFIQNVILVFFCVGMIAGVFPWFLVAV 1018
           || |||||||||:|||||||||:|||||| || |:|   :| | : ::| |||  |: |
Db     893 PMSFFDTTPTGRLMNRFSKDMDELDVRLPFHAENFLQQFFMVVFILVILAAVFPAVLLVV 952

Qy    1019 GPLVILFSVLHIVSRVLIRELKRLDNITQSPFLSHITSSIQGLATIHAYNKGQEFLHRYQ 1078
           | : | :|  :    ::|||:::|:::||: :|||||:|||  |||| | :  :
Db     953 ASLAVGFFILLRIFHRGVQELKKVENVSRSPWFTHITSSMQGLGIIHAYGKKESCI---T 1009

Qy    1079 ELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGLMIVLMHGQIPPAYAGLAISYAVQ 1138
           | |:| :    | ||:|| |:|:|::   | |  |:: |    | :  ||::|| :|
Db    1010 TLNDENSSHLLYFNCALRWFALRMDVLMNILTFTVALLVTLSFSSISTSSKGLSLSYIIQ 1069

Qy    1139 LTGLFQFTVRLASETEARFTSVERINHYIKTLSLEAPARIKNKAPSPDWPQEGEVTFENA 1198
           |:|| |  ||  :||:|:|||||  :  || |   |    :|      |||  ||:|| :
Db    1070 LSGLLQVCVRTGTETQAKFTSVELLREYISTCVPECTHPLKVGTCPKDWPSXGEITFRDY 1129

Qy    1199 EMRYRENLPLVLKKVSFTIKPKEKIGIVGRTGSGKSSLGMALFRLVELSGGCIKIDGVRI 1258
           :||||:| ||||  ::  |:  : :|||||||||||||||||||||| : | | || | |
Db    1130 QMRYRDNTPLVLDSLNLNIQSGQTVGIVGRTGSGKSSLGMALFRLVEPASGTIFIDEVDI 1189

Qy    1259 SDIGLADLRSKLSIIPQEPVLFSGTVR 1285
           : | |||:||::|||:|||| ||||
Db    1190 CILSLEDLRTKLTVIPQDPVLFVGTVR 1216
```

Search completed: August 11, 2002, 11:12:12
Job time: 6682 sec